


```

Db 84 ARYPTDSKGGKYSALIEIQONATTGCKYAPLKTNYNSLGADDLTPGCEQLVNSGKIF 143
QY 121 YRVESLTRNIVPFRSSGSRVIAKGFIEGQSTKLKDPRAQPGOSSPKIDVWISA 180
Db 144 YRVESLTRNIIIPFRSSGSRVIAKGFIEGQSTKLKDPRAQPGOSSPKIDVWISA 203
QY 181 SSSNNTLDPGCTCTVFEDSELADVEANFTATVPFSIRORLENDLSGVTCTDEVTYLM 240
Db 204 SSSNNTLDPGCTCTVFEDSELADVEANFTATVPFSIRORLENDLSGVTCTDEVTYLM 263
QY 241 CSFDTISTSTVDTKLSFPCDLFTHEMINYDYQLSLKYYKHGAGNPLGPTQGVYAN 300
Db 264 CSFDTISTSTVDTKLSFPCDLFTHEMINYDYQLSLKYYKHGAGNPLGPTQGVYAN 323
QY 301 IARLTHSPVHDDTSSNHTLDSNPATPLNSTLYADFSHNGIISILFALGLYNGTKPL 360
Db 324 IARLTHSPVHDDTSSNHTLDSNPATPLNSTLYADFSHNGIISILFALGLYNGTKPL 383
QY 361 TTVENITQTDGFSSAWTVFPFASRLYVENMQCAQEQLVRLVNDRVLPVPHGCPVDA 420
Db 384 TTQVNIQTQDGFSSAWTVFPFASRLYVENMQCAQEQLVRLVNDRVLPVPHGCPVDA 443
QY 421 CTRDSFVRGLSFARSGGDWAECEFA 444
Db 444 CTRDSFVRGLSFARSGGDWAECEFA 467

RESULT 2
Q8J255 PRELIMINARY; PRT: 448 AA.
AC Q8J255
DT C1-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Phytase (Fragment).
GN PHA.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5058;
RN [1]
RP SEQUENCE FROM N.A.
RA Li G., Zhu J., Sun J., Wu Z., Wang L., Chen G., Jiang H., Li M.;
RI Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF537344; AAK10115.1; -
FT NON-TER
SQ SEQUENCE 448 AA; 49260 MW; 0554FF9712FF7BAA CRC64;

Query Match 96.8%; Score 2260; DB 3; Length 448;
Best Local Similarity 95.5%; Pred. No. 7.4e-165;
Matches 424; Conservative 14; Mismatches 6; Indels 0; Gaps 0;

QY 1 ASRNCSCDVTDOGYCCFSETSHLWQYAPFSLANESVISPVPAGCRVTFQAVLSRHG 60
Db 5 ASRNCSCDVTDOGYCCFSETSHLWQYAPFSLANESVISPVPAGCRVTFQAVLSRHG 64
QY 61 ARYPTDSKGGKYSALIEIQONATTGCKYAPLKTNYNSLGADDLTPGCEQLVNSGKIF 120
Db 65 ARYPTDSKGGKYSALIEIQONATTGCKYAPLKTNYNSLGADDLTPGCEQLVNSGKIF 124
QY 121 YRVESLTRNIVPFRSSGSRVIAKGFIEGQSTKLKDPRAQPGOSSPKIDVWISA 180
Db 125 YRVESLTRNIVPFRSSGSRVIAKGFIEGQSTKLKDPRAQPGOSSPKIDVWISA 184
QY 181 SSSNNTLDPGCTCTVFEDSELADVEANFTATVPFSIRORLENDLSGVTCTDEVTYLM 240
Db 185 STSNKTLDPGCTCTVFEDSELADVEANFTATVPFSIRORLENDLSGVTCTDEVTYLM 244
QY 241 CSFDTISTSTVDTKLSFPCDLFTHEMINYDYQLSLKYYKHGAGNPLGPTQGVYAN 300
Db 245 CSFDTISTSTVDTKLSFPCDLFTHEMINYDYQLSLKYYKHGAGNPLGPTQGVYAN 304
QY 301 IARLTHSPVHDDTSSNHTLDSNPATPLNSTLYADFSHNGIISILFALGLYNGTKPL 360

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Db 305 IARLTHSPVHDDTSSNHTLDSNPATPLNSTLYADFSHNGIISILFALGLYNGTKPL 364
QY 361 TTVENITQTDGFSSAWTVFPFASRLYVENMQCAQEQLVRLVNDRVLPVPHGCPVDA 420
Db 365 TTAENITQTDGFSSAWTVFPFASRLYVENMQCAQEQLVRLVNDRVLPVPHGCPVDA 424
QY 421 CTRDSFVRGLSFARSGGDWAECEFA 444
Db 425 CTRDSFVRGLSFARSGGDWAECEFA 448

RESULT 3
Q93838 PRELIMINARY; PRT: 467 AA.
AC Q93838
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Phytase.
GN PHA.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP SEQUENCE FROM N.A.
RA Nagashima T., Kondo H., Anazawa H., Terasaki Y.;
RI "Phytase having high-affinity for phytic acid.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB022700; BAA74433.1; -
DR HSSP: P34752; 1IHP.
DR InterPro: IPR000560; HisAc_phsphtse.
DR Pfam: PF00328; acid_phosphat_1.
DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.
DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.
SQ SEQUENCE 467 AA; 51028 MW; 7A38AD543EDC265C CRC64;

Query Match 96.8%; Score 2259; DB 3; Length 467;
Best Local Similarity 95.3%; Pred. No. 9.4e-165;
Matches 423; Conservative 14; Mismatches 7; Indels 0; Gaps 0;

QY 1 ASRNCSCDVTDOGYCCFSETSHLWQYAPFSLANESVISPVPAGCRVTFQAVLSRHG 60
Db 24 ASRNCSCDVTDOGYCCFSETSHLWQYAPFSLANESVISPVPAGCRVTFQAVLSRHG 83
QY 61 ARYPTDSKGGKYSALIEIQONATTGCKYAPLKTNYNSLGADDLTPGCEQLVNSGKIF 120
Db 84 ARYPTDSKGGKYSALIEIQONATTGCKYAPLKTNYNSLGADDLTPGCEQLVNSGKIF 143
QY 121 YRVESLTRNIVPFRSSGSRVIAKGFIEGQSTKLKDPRAQPGOSSPKIDVWISA 180
Db 144 YRVESLTRNIVPFRSSGSRVIAKGFIEGQSTKLKDPRAQPGOSSPKIDVWISA 203
QY 181 SSSNNTLDPGCTCTVFEDSELADVEANFTATVPFSIRORLENDLSGVTCTDEVTYLM 240
Db 204 STSNKTLDPGCTCTVFEDSELADVEANFTATVPFSIRORLENDLSGVTCTDEVTYLM 263
QY 241 CSFDTISTSTVDTKLSFPCDLFTHEMINYDYQLSLKYYKHGAGNPLGPTQGVYAN 300
Db 264 CSFDTISTSTVDTKLSFPCDLFTHEMINYDYQLSLKYYKHGAGNPLGPTQGVYAN 323
QY 301 IARLTHSPVHDDTSSNHTLDSNPATPLNSTLYADFSHNGIISILFALGLYNGTKPL 360
Db 324 IARLTHSPVHDDTSSNHTLDSNPATPLNSTLYADFSHNGIISILFALGLYNGTKPL 383
QY 361 TTVENITQTDGFSSAWTVFPFASRLYVENMQCAQEQLVRLVNDRVLPVPHGCPVDA 420
Db 384 TTAENITQTDGFSSAWTVFPFASRLYVENMQCAQEQLVRLVNDRVLPVPHGCPVDA 443
QY 421 CTRDSFVRGLSFARSGGDWAECEFA 444

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Db 444 CTRDSFVKGLSFARSGDNGWCEFA 467
RESULT 4
ID Q9HEQ0 PRELIMINARY; PRT; 467 AA.
AC Q9HEQ0
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Phytase.
OS Aspergillus ficuum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5058;
RN [1]
RJ EMBL; AV013315; AAG40885.1; -.
CR HSSP; P34752; 1HP.
DR InterPro; IPR000560; HisAc_phsphtse.
DR Pfam; PF00328; acid_phosphat_1; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
SQ SEQUENCE 467 AA; 51012 MW; 3F695D543C0B555B CRC64;
Query Match: 96.4%; Score 2249; DB 3; Length 467;
Best Local Similarity 95.3%; Pred. No. 5.9e-164;
Matches 423; Conservative 14; Mismatches 17; Indels 0; Gaps 0;
QY 1 ASRNQSCDTVDQGYQCFSETSLHWGQYAPFPFSUANESVISPEVAGCRVTFAQVLSRHG 63
DB 24 ASRNQSCDTVDQGYQCFSETSLHWGQYAPFPFSUANESVISPEVAGCRVTFAQVLSRHG 83
QY 61 ARYPTDSKGGKYSALIEIICQNTATFGKYAFPLKTYNSLGAADLTTPFGEQELVNSGKIF 120
DB 84 ARYPTDSKGGKYSALIEIICQNTATFGKYAFPLKTYNSLGAADLTTPFGEQELVNSGKIF 143
QY 121 YQYESLTRNIVFPFIRSSGSRVIAAGKFEIEGQSTKLKDPRAQGGSPKIDVVISPA 180
DB 144 YQYESLTRNIVFPFIRSSGSRVIAAGKFEIEGQSTKLKDPRAQGGSPKIDVVISPA 203
QY 161 SSSNNTLDPGCTVFESELAADTVEANFTATFVPSIRQRLNDLSGVTLTDEVTYMDM 240
DB 204 STSNNTLDPGCTVFESELAADTVEANFTATFVPSIRQRLNDLSGVTLTDEVTYMDM 263
QY 241 CSFDTISTSTVDTKLSPFCDLFTHEWINDYLSLKKYKHGAGNPLGPTQGVYANEL 300
DB 264 CSFDTISTSTVDTKLSPFCDLFTHEWINDYLSLKKYKHGAGNPLGPTQGVYANEL 323
QY 301 IARLTHSPVHDDTSSNHTLDSSEPATPLNSTLYADFSHONGIISILFALGLYNGTKPLST 360
DB 324 IARLTHSPVHDDTSSNHTLDSSEPATPLNSTLYADFSHONGIISILFALGLYNGTKPLST 383
QY 361 TVENITQDGFSSAWTVFPASRLYVEMQCEQEPFLRVLVNDRVVPVHGCPVDALGR 420
DB 384 TTAENITQDGFSSARTVFPASRLYVEMQCEQEPFLRVLVNDRVVPVHGCPVDALGR 443
QY 421 CTRDSFVKGLSFARSGDNGWCEFA 444
DB 444 CTRDSFVKGLSFARSGDNGWCEFA 467
RESULT 5
Q9C1T1 PRELIMINARY; PRT; 466 AA.
ID Q9C1T1
AC Q9C1T1
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Phytase.
OS Aspergillus fumigatus (Sartorya fumigata).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5085;
RN [1]
RJ EMBL; AB042805; BAB40715.1; -.
CR HSSP; P34752; 1HP.
DR InterPro; IPR000560; HisAc_phsphtse.
DR Pfam; PF00328; acid_phosphat_1; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
SQ SEQUENCE 466 AA; 51257 MW; 8033BED57FBA2791 CRC64;
Query Match: 69.0%; Score 1610; DB 3; Length 466;
Best Local Similarity 67.0%; Pred. No. 5.1e-115;
Matches 297; Conservative 57; Mismatches 89; Indels 0; Gaps 0;
QY 2 SRNQSCDTVDQGYQCFSETSLHWGQYAPFPFSUANESVISPEVAGCRVTFAQVLSRHGA 61
DB 24 SRNQSCDTVDQGYQCFSETSLHWGQYAPFPFSUANESVISPEVAGCRVTFAQVLSRHGA 83
QY 62 RYPTDSKGGKYSALIEIICQNTATFGKYAFPLKTYNSLGAADLTTPFGEQELVNSGKIF 121
DB 84 RYPTDSKGGKYSALIEIICQNTATFGKYAFPLKTYNSLGAADLTTPFGEQELVNSGKIF 143
QY 122 QYVESLTRNIVFPFIRSSGSRVIAAGKFEIEGQSTKLKDPRAQGGSPKIDVVISPA 181
DB 144 QYVESLTRNIVFPFIRSSGSRVIAAGKFEIEGQSTKLKDPRAQGGSPKIDVVISPA 203
QY 182 SSSNNTLDPGCTVFESELAADTVEANFTATFVPSIRQRLNDLSGVTLTDEVTYMDM 241
DB 204 GFNNTLDHSLCTAFENSTTGDDADCKFTAVFTPSIVERLEKCLPGTLLSSKEVYVMDMC 263
QY 242 SFDTISTSTVDTKLSPFCDLFTHEWINDYLSLKKYKHGAGNPLGPTQGVYANELI 301
DB 264 SFDTISTSTVDTKLSPFCDLFTHEWINDYLSLKKYKHGAGNPLGPTQGVYANELI 323
QY 302 IARLTHSPVHDDTSSNHTLDSSEPATPLNSTLYADFSHONGIISILFALGLYNGTKPLST 361
DB 324 IARLTHSPVHDDTSSNHTLDSSEPATPLNSTLYADFSHONGIISILFALGLYNGTKPLST 383
QY 362 TVENITQDGFSSAWTVFPASRLYVEMQCEQEPFLRVLVNDRVVPVHGCPVDALGR 421
DB 384 SVQSTETNGYSSARTVFPGARAYVEMQCEQEPFLRVLVNDRVVPVHGCPVDALGR 443
QY 422 TRDSFVKGLSFARSGDNGWCEFA 444
DB 444 KRDDFVGLSFTVSGNNGCEFA 466
RESULT 6
OC0092 PRELIMINARY; PRT; 465 AA.
ID OC0092
AC OC0092
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 3-phytase A precursor (EC 3.1.3.8) (MYO-inositol-hexaphosphate 3-phosphohydrolase A) (3 phytase A) (MYO-inositol hexakisphosphate phosphohydrolase A).
DE PHA.
OS Aspergillus fumigatus (Sartorya fumigata).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5085;
RN [1]
RJ EMBL; AB042805; BAB40715.1; -.
CR HSSP; P34752; 1HP.
DR InterPro; IPR000560; HisAc_phsphtse.
DR Pfam; PF00328; acid_phosphat_1; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
SQ SEQUENCE 466 AA; 51257 MW; 8033BED57FBA2791 CRC64;
Query Match: 69.0%; Score 1610; DB 3; Length 466;
Best Local Similarity 67.0%; Pred. No. 5.1e-115;
Matches 297; Conservative 57; Mismatches 89; Indels 0; Gaps 0;
QY 2 SRNQSCDTVDQGYQCFSETSLHWGQYAPFPFSUANESVISPEVAGCRVTFAQVLSRHGA 61
DB 24 SRNQSCDTVDQGYQCFSETSLHWGQYAPFPFSUANESVISPEVAGCRVTFAQVLSRHGA 83
QY 62 RYPTDSKGGKYSALIEIICQNTATFGKYAFPLKTYNSLGAADLTTPFGEQELVNSGKIF 121
DB 84 RYPTDSKGGKYSALIEIICQNTATFGKYAFPLKTYNSLGAADLTTPFGEQELVNSGKIF 143
QY 122 QYVESLTRNIVFPFIRSSGSRVIAAGKFEIEGQSTKLKDPRAQGGSPKIDVVISPA 181
DB 144 QYVESLTRNIVFPFIRSSGSRVIAAGKFEIEGQSTKLKDPRAQGGSPKIDVVISPA 203
QY 182 SSSNNTLDPGCTVFESELAADTVEANFTATFVPSIRQRLNDLSGVTLTDEVTYMDM 241
DB 204 GFNNTLDHSLCTAFENSTTGDDADCKFTAVFTPSIVERLEKCLPGTLLSSKEVYVMDMC 263
QY 242 SFDTISTSTVDTKLSPFCDLFTHEWINDYLSLKKYKHGAGNPLGPTQGVYANELI 301
DB 264 SFDTISTSTVDTKLSPFCDLFTHEWINDYLSLKKYKHGAGNPLGPTQGVYANELI 323
QY 302 IARLTHSPVHDDTSSNHTLDSSEPATPLNSTLYADFSHONGIISILFALGLYNGTKPLST 361
DB 324 IARLTHSPVHDDTSSNHTLDSSEPATPLNSTLYADFSHONGIISILFALGLYNGTKPLST 383
QY 362 TVENITQDGFSSAWTVFPASRLYVEMQCEQEPFLRVLVNDRVVPVHGCPVDALGR 421
DB 384 SVQSTETNGYSSARTVFPGARAYVEMQCEQEPFLRVLVNDRVVPVHGCPVDALGR 443
QY 422 TRDSFVKGLSFARSGDNGWCEFA 444
DB 444 KRDDFVGLSFTVSGNNGCEFA 466
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RA Pasamontes L., Haiker M., Wyss M., Tessier M., van Loon A.P.G.M.;
 RT "Gene cloning, purification, and characterization of a heat-stable
 RL phytase from the fungus *Aspergillus fumigatus*."; Appl. Environ. Microbiol. 63:1596-1700(1997).
 CC -1- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
 CC FROM PHYTATE.
 CC -1- CATALYTIC ACTIVITY: MYO-INSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-
 CC INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- MISCELLANEOUS: SHOWS HIGH ACTIVITY WITH 4-NITROPHENYL PHOSPHATE AT
 CC A PH RANGE OF 3 TO 5 AND WITH PHYTIC ACID AT A PH RANGE OF 2.5 TO
 CC 7.5. IT IS ABLE TO WITHSTAND TEMPERATURES UP TO 100 DEGREES
 CC CELSIUS OVER A PERIOD OF 20 MIN, WITH A LOSS OF ONLY 10% OF THE
 CC INITIAL ENZYMIC ACTIVITY.
 CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 CC EMBL: U59804; AAB96872.1; -.
 DR HSP; P34752; 1:HP.
 DR InterPro: IPR000560; HisAc_phsphtse.
 DR Pfam: PF00328; acid_phosphat_1.
 DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.
 DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.
 KW Hydrolase; Glycoprotein; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 465
 FT ACT_SITE 81 81
 FT ACT_SITE 82 82
 FT ACT_SITE 359 359
 FT DISULFID 30 39
 FT DISULFID 70 412
 FT DISULFID 213 463
 FT DISULFID 262 280
 FT DISULFID 434 442
 FT CARBOHYD 104 119
 FT CARBOHYD 119 119
 FT CARBOHYD 205 205
 FT CARBOHYD 228 228
 FT CARBOHYD 337 337
 FT CARBOHYD 350 350
 FT CARBOHYD 374 374
 SQ SEQUENCE 465 AA; 50836 MW; 86FC1D9058C9B2C9 CRC64;
 Query Match 68.8%; Score 1606.5; DB 3; Length 465;
 Best Local Similarity 66.4%; Pred. No. 9.4e-115;
 Matches 295; Conservative 59; Mismatches 89; Indels 1; Gaps 1;
 QY 1 ASRQSCDVTVOGQYCFSTSLHWQYAPFFSLANESVISPEVAGCRVTPAQVLSRHG 60
 DB 23 SSAGSKCDTVLQYQCSPTSLHWQYSPFFSLEDELSVSKLPKDCRITLVQVLSRHG 82
 QY 61 ARYPTDSKGYKYSALISECCNATTFDQKPAFLKTYNYSLGADDLTPPGQELVNSGTFK 120
 DB 83 ARYPTSSKKYKYLKVAIQANATDFKGPAPFLKTYNYTLGADDLTPPGQELVNSGTFK 142
 QY 121 YQYESLTRNIVPFISSSSSRVSIASGKFFIEGQSTKLKDPRAQGGSSPKIDVWISAE 180
 DB 143 YQYKALARSVVPFIRASGSDRVSIASGKFFIEGQCAKLADPGA-TNRAAPAIISVIIPE 201
 QY 181 SSSNNTLDPGCTVFEDSELDVVENATFVPSIRORLENDLSGVTLTCTETVLMQY 240
 DB 202 ETFNNTLDHGVCYKFEASQSGDEVAANFTALFAPDIRARAEKHLPGVTLTDEVDVSLMDM 261
 QY 241 CSFTTISTSTVDTKLSPPFCOLFHDENINYDYLQSLKYYGAGNPLGPTQGVGYANEL 300
 DB 262 CSFTVARTSDAQLSPFCOLFTHNEWKYNVLSLGYGYGAGNPLGPAQGIQFTNEL 321
 QY 301 IARLTHSPVHDTSSNHTLDSSPATFPNLTLYADFSHNGIISILFALGLYNGTKPLST 360
 DB 322 IARLTRSPVQDHTSTNSTLVSNPATFPNLATWYVDFSHDMSVSIFFALGLYNGTEPLSR 381
 QY 361 TTVENITCTDGFSSAMTVPFASLYVEMMOCAEQELPLRVLVNDRVPLHCCPVDALGR 420
 DB 382 TSVESAKELDQYSASWVVPFGARAYFETMCKSEKEPLVRALINDRVVPLHGCCVDKLG 441

QY 421 CTRDSFVRGSLSPARSGGDWAECPA 444
 DB 442 CKLNDVFKGLSWARSGGNWGECS 455
 RESULT 7
 Q8WZJ5
 ID Q8WZJ5 PRELIMINARY; PRT; 442 AA.
 AC Q8WZJ5;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Phytase (EC 3.1.3.8, precursor (Fragment)).
 GN PH1A3.
 CC *Aspergillus fumigatus* (Sartorya fumigata).
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurctiomycetes;
 CC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5085;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CCCTCC AF93024;
 RA Zhang G.;
 RT "Cloning of phytase gene from *Aspergillus fumigatus* and its expression
 RT in *Pichia pastoris*."; Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AJ419776; CAD12029.1; -.
 DR InterPro: IPR000560; HisAc_phsphtse.
 DR Pfam: PF00328; acid_phosphat_1.
 DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.
 DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.
 KW Signal; Hydrolase.
 FT SIGNAL 1 1
 FT NON_TER 1 1
 FT CHAIN 4 442
 FT SEQUENCE 442 AA; 48485 MW; 3FDBAC656A268514 CRC64;
 Query Match 68.8%; Score 1605.5; DB 3; Length 442;
 Best Local Similarity 66.6%; Pred. No. 1e-114;
 Matches 295; Conservative 58; Mismatches 89; Indels 1; Gaps 1;
 QY 2 SRNQSCDVTVOGQYCFSTSLHWQYAPFFSLANESVISPEVAGCRVTPAQVLSRHGA 61
 DB 1 SAGSKCDTVLQYQCSPTSLHWQYSPFFSLEDELSVSKLPKDCRITLVQVLSRHGA 60
 QY 62 RYPTDSKGYKYSALISECCNATTFDQKPAFLKTYNYSLGADDLTPPGQELVNSGTFK 121
 DB 61 RYPTSSKKYKYLKVAIQANATDFKGPAPFLKTYNYTLGADDLTPPGQELVNSGTFK 120
 QY 122 QRYESLTRNIVPFISSSSSRVSIASGKFFIEGQSTKLKDPRAQGGSSPKIDVWISAE 181
 DB 121 QRYKALARSVVPFIRASGSDRVSIASGKFFIEGQCAKLADPGA-TNRAAPAIISVIIPE 179
 QY 192 SSSNNTLDPGCTVFEDSELDVVENATFVPSIRORLENDLSGVTLTCTETVLMQY 241
 DB 180 ETFNNTLDHGVCYKFEASQSGDEVAANFTALFAPDIRARAEKHLPGVTLTDEVDVSLMDM 239
 QY 242 SFTTISTSTVDTKLSPPFCOLFHDENINYDYLQSLKYYGAGNPLGPTQGVGYANEL 301
 DB 240 SFTVARTSDAQLSPFCOLFTHNEWKYNVLSLGYGYGAGNPLGPAQGIQFTNEL 299
 QY 302 IARLTHSPVHDTSSNHTLDSSPATFPNLTLYADFSHNGIISILFALGLYNGTKPLST 361
 DB 300 IARLTRSPVQDHTSTNSTLVSNPATFPNLATWYVDFSHDMSVSIFFALGLYNGTEPLSR 359
 QY 362 TTVENITCTDGFSSAMTVPFASLYVEMMOCAEQELPLRVLVNDRVPLHCCPVDALGR 421
 DB 360 TSVESAKELDQYSASWVVPFGARAYFETMCKSEKEPLVRALINDRVVPLHGCCVDKLG 419
 QY 422 TRDSTFVRGSLSPARSGGDWAECPA 444
 DB 420 KUNDVFKGLSWARSGGNWGECS 442

RESULT 8

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000100
ID C00100 PRELIMINARY; PRT; 466 AA.
AC C00100;
DT 01-JUL-1997 (TREMBlrel. 04, Created);
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update);
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update);
DE 3-phosphate precursor (EC 3.1.3.8) (MYO-inositol-hexaphosphate 3-phosphohydrolase) (3 phytase) (MYO-inositol hexakisphosphate phosphohydrolase);
DE Aspergillus terreus;
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=33178;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=CBS 116.46;
RA Pasamontes L., Haiker M., Henriquez Huecas M., Hug D., Mitchell D.B.,
RA Broger C., van Loon A.P.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE FROM PHYTATE (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
DR EMBL: U60412; AAB58465.1; -.
DR HSSP: P34752; 1IHP.
DR InterPro: IPR000560; HisAc_pshptase.
DR Pfam: PF00328; acid phosphat.
DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW Hydrolase; Glycoprotein; Signal.
FT SIGNAL 1 15 POTENTIAL.
FT CHAIN 16 466 3-PHYTASE.
FT ACT_SITE 82 82 REQUIRED FOR BINDING SUBSTRATE (BY SIMILARITY).
FT ACT_SITE 83 83 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
FT ACT_SITE 361 361 PROTON DONOR (BY SIMILARITY).
FT DISULFID 31 40 BY SIMILARITY.
FT DISULFID 71 414 BY SIMILARITY.
FT DISULFID 215 465 BY SIMILARITY.
FT DISULFID 264 282 BY SIMILARITY.
FT DISULFID 436 444 BY SIMILARITY.
FT CARBOHYD 27 27 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 105 105 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 120 120 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 207 207 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 376 376 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 466 AA; 51055 MW; F2AECACAF7C22C4 CRC64;

Query Match 65.1%; Score 1520; DB 3; Length 466;
Best Local Similarity 63.4%; Pred. No. 4e-108;
Matches 279; Conservative 65; Mismatches 96; Indels 0; Gaps 0;

QY 4 NQSCDVTVDGQYQCFSSTSLHWGQYAPFFSLANESVISPVPAGCRVTFPAQVSRHGARY 63
D 27 NNSDCTSVDRGQYCFPELSHKWLGYAPYPSLQDESPPFLDVPDCHITFVQVLAHGRAS 86
QY 64 PTDSKGGKYSALIEIQONATTFDCKYAFKTYNYSLGADLTLPFGCEGLVNSGKIFYOR 123
D 87 PTDSKTKAYAAATAAIQKNATAJPGKAFKLSYNSMGSENLPFGNQLQDLGACFYRR 146
QY 124 YESITRNIVPPIRSSGSSRVIASGKKFEGFQSTKADPRAQCGOSSPKIDVVISASSS 193
D 147 YDTLIRHINPVRADSSRVHSEKFEVGFQNGARQCDPANHQPSPRVDDVWIPGATY 206
QY 184 NNTLDPGCTVFDESELADTVEANFTATFVPSIRQRLENDLSGVTLTDEVTYLMDCSP 243

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DB 207 NNTLEHSICTAFEASTVGDAAADNFTAVFAPAIKRLEADLPGLVQLSADDDVNLXAMCFF 266
QY 244 DTISTSTVDTKLSPFCDLFTHEWINYDYQSLKKYGHGAGNPGPTQGVGYANELLAR 303
D 267 ETVSILTDDAHTLSPFCDLFTAAEKTYNYLLSLDKYGGGNGPLGPGVQGVGMANEJLAR 326
QY 304 LTHSPVHDDTSSNHTLSSSPATFPLNSTLYADFSHGNGIISILFALGLYNTKPKLSTTV 363
D 327 LTRSPVHDDTSSNHTLSSSPATFPLNSTLYADFSHGNGIISILFALGLYNTKPKLSTTV 386
QY 364 ENITOTQCFSSAWTPFASRLYVEMQCAOEPLVRLVNDRVVPJGCPVDCALGRCTR 423
D 397 EDITRTDGYAAAWTPFAARAYIEMMQCAOEPLVRLVNDRVVPJGCPVDCALGRCTR 446
QY 424 DSFVRGLSFAIRSGSDWAECP 443
D 447 DDFVEGLSFARAGGNWAECP 466

RESULT 9
000096 PRELIMINARY; PRT; 466 AA.
ID C00096;
AC C00096;
DT 01-JUL-1997 (TREMBlrel. 04, Created);
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update);
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update);
DE Phytase (EC 3.1.3.8);
DE Talaromyces thermophilus.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Talaromyces.
OX NCBI_TaxID=28565;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=98007872; PubMed=9349716;
RA Pasamontes L., Haiker M., Henriquez Huecas M., Mitchell D.B.,
RA van Loon A.P.;
RL "Cloning of the phytases from Emericella nidulans and the thermophilic fungus Talaromyces thermophilus.";
RL Biochim. Biophys. Acta 1353:217-223 (1997).
DR EMBL: U59402; AAB96873.1; -.
DR HSSP: P34752; 1IHP.
DR InterPro: IPR000560; HisAc_pshptase.
DR Pfam: PF00328; acid phosphat.
DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW Hydrolase.
SQ SEQUENCE 466 AA; 51450 MW; FC4575B521A5C929 CRC64;

Query Match 64.1%; Score 1496.5; DB 3; Length 466;
Best Local Similarity 62.2%; Pred. No. 2.5e-106;
Matches 278; Conservative 59; Mismatches 106; Indels 5; Gaps 2;

QY 2 SRN----OSSCDTVDGQYQCFSSTSLHWGQYAPFFSLANESVISPVPAGCRVTFPAQVLS 57
D 18 SRNPHVDSHSNTVEGGYQCRPEISHSWGQYSPFFSLADQSEISPDVPQNCKITFVQLLS 77
QY 58 RHGARYPTDSKGGKYSALIEIQONATTFDCKYAFKTYNYSLGADLTLPFGCEGLVNSG 117
D 78 RHGARYPTDSKGGKYSALIEIQONATTFDCKYAFKTYNYSLGADLTLPFGCEGLVNSG 137
QY 118 IKFYORVESLIRNIVPPIRSSGSSRVIASGKKFEGFQSTKADPRAQCGOSSPKIDVVI 177
D 138 IKFYNHYSKLARNVPPFVRCSSDRVIASGRFLFIEGFQSAKVLDPHSDKDCAPTINVII 197
QY 178 SEASSNNTLDPGCTVFDESELADTVEANFTATFVPSIRQRLENDLSGVTLTDEVTYL 237
D 198 EGGPSYNTLDTGSCPVEDSSGCGHDAQEKFAKAPALIEKIKDHLPGVGLAVSDVPV 257
QY 238 NDMCSFDITISTSTVDTKLSPFCDLFTHEWINYDYQSLKKYGHGAGNPLGPTQGVGYA 297
D 258 MDLCPEFTLARNHDTLSPEFCAJSTOBEWQAYDYQSLGKYGNGGNGNPLGPAQGVGFV 316
QY 298 NELIARLTHSPVHDDTSSNHTLSSSPATFPLNSTLYADFSHGNGIISILFALGLYNTKPK 357

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FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 442 PHYTASE.
SQ SEQUENCE 442 AA; 47915 MW; 046401C69:D86702 CRC64;

Query Match 31.7%; Score 739; DB 3; Length 442;
Best Local Similarity 45.0%; Pred. No. 2.6e-48;
Matches 175; Conservative 64; Mismatches 154; Indels 34; Gaps 14;

QY 25 WGVYAPFSLANESVISPEVAGGRVTFPAQVLSRHGARYPTDSGGKYSALEIEIQ--QN 82
DB 40 WSPYSVPFPLAEYKA---PPAGCQINQVNIQRHGAEFP--SGATTRIKAGLTKLGQVN 95
QY 83 ATTFDGYAFELKTYNSLGAADDLTPFGDELVNSG--KFYQYES--TNTVFFIRSSQSS 141
DB 96 FTD--DAKFNZTKSEFYDIGNSLVFPGAQCFDAGQEAFAFYSLKLVKNLPTFRAQSC 153
QY 142 RVIASGKKFISGFSTKJKDPPAQPGQSSPKIDVVISSEASSNNTDPGTCTVDESELA 201
DB 154 RVDSATNWTAGFAS-----ASHNTVQPKNLILPQ--TGNDTLENNCPALGDS-- 202
QY 202 DTVEANFTATTFVSIROPLENDLSGVTITDTETVYLMDCMCFDTISTVTKLSFFQDL 261
DB 203 PQYVAMJAVAF--PSITARLNAAAFSVNLTD--DAFN--VSLCAFLVSKS---KXSCFCTL 257
QY 262 F--THDSWINDYQLCSKKYIGHGAGNPLGTQGVGYANEIARLTHSPVEDTSSNHTI 319
DB 258 FEGIPGFPAFAYGDDLKFKYGTGYGQELGPVQGVGYVNELIARLTNSAVRCNTQTNRIL 317
QY 320 DSSPATPLNSTLYADPSHDNGIISLFAELGYNGTKPLSTTYENTCTDGFSSAKVTP 379
DB 318 CASPVITPLKNTFFYADPSHCLMNAVFSAMGJFQPAPLS--TSVNPARTWTSS--LVP 374
QY 380 FASRLYIYEMNCCQAEQEP--VRVLVNDRVVPLFGGCPVDALGCRTRDSSFYGLSLFARS--GG 437
DB 375 FSGRMWVERLSCFGTKK--VRVLQDVQVPLEFCGDRNGLCTLAKPFVSTQFAPSCAG 432
QY 438 DWATCFCA 444
DB 433 DFEKCFCA 439

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Search completed: November 12, 2003, 14:32:48
Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 12, 2003, 14:26:15 ; Search time 17 Seconds
(without alignments)
1228.227 Million cell updates/sec

Title: US-10-062-848-1
Perfect score: 2334
Sequence: 1 ASRQSSCDTVQGIQCFSE.....SFRG:SPARSGDWAECA 444

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2334	100.0	467	PHYA_ASPNG	P34752 aspergillus
2	2290	98.1	467	PHYA_ASPNG	P34753 aspergillus
3	1532.5	65.7	463	PHYB_ENENI	Q00093 emeritella
4	385	16.5	467	PPA3_YEAST	Q20031 saccharomyc
5	385	16.5	467	PPA5_YEAST	PC5635 saccharomyc
6	368	15.8	468	PPAD_YEAST	P52290 saccharomyc
7	352	15.1	467	PPAB_YEAST	P35842 saccharomyc
8	352	15.1	467	PPAC_YEAST	P38693 saccharomyc
9	351	15.0	469	PPA5_KLJLA	P52289 kluyveromyc
10	339.5	14.5	479	PHYB_ASPNG	P34754 aspergillus
11	336.5	14.4	479	PHYB_ASPNG	P34755 aspergillus
12	327	14.0	468	PPA1_PICPA	P52252 pichia past
13	296.5	12.7	453	PPA1_SCHPO	P08091 schizosacch
14	284	12.2	463	PPA2_SCHPO	Q01682 schizosacch
15	119.5	5.1	413	AGP_ECOLI	P19926 escherichia
16	115	4.9	590	PEPF_BORBU	O51264 borrelia bu
17	109.5	4.7	413	AGP_SALTY	O33921 salmonella
18	107	4.6	2314	PTP2_HUMAN	P23471 homo sapien
19	106	4.5	507	RRPF_CDOG	P36940 canine dist
20	106	4.5	755	PPAX_CAEEL	Q09549 caenorhabdi
21	105.5	4.5	422	PPAY_CAEEL	Q10944 caenorhabdi
22	104.5	4.5	1254	UBPC_YEAST	P39538 saccharomyc
23	104	4.5	504	CP12_RAT	P05183 rattus norv
24	104	4.5	1306	MSB2_YEAST	P32334 saccharomyc
25	102	4.4	927	CC15_SCHPO	Q09522 schizosacch
26	101.5	4.3	421	PPAL_MOUSE	P24638 mus musculu
27	101	4.3	667	Y431_HUMAN	Q43313 homo sapien
28	101	4.3	677	NRG1_XENLA	Q93383 xenopus lae
29	100.5	4.3	936	PMPT_CHJPN	Q28988 chlamydia p
30	99.5	4.3	658	LITB_STRPN	P59205 streptococc
31	99	4.2	567	CH13_CANAL	P40354 candida alb
32	98.5	4.2	423	PPAL_RAT	P20611 rattus norv
33	98	4.2	423	PPAL_HUMAN	P11117 homo sapien

ALIGNMENTS

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RESULT 1
PHYA_ASPNG
ID PHYA_ASPNG STANDARD; PRT; 467 AA.
AC P34752;
DI 01-FEB-1994 (Rel. 28, Created)
DI 01-FEB-1994 (Rel. 28, Last sequence update);
DI 15-SEP-2003 (Rel. 42, Last annotation update);
DE 3-phytase A precursor (EC 3.1.3.8) (Myo-inositol-hexaphosphate
DE 3-phosphorylase A); (3 phytase A) (Myo-inositol hexakisphosphate
DE 3-phosphohydrolase A);
GN PHYA.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=NRRL 3135 / VAN TIEGHEM / FICUUM;
RX MEDLINE=93252284; PubMed=8387447;
RA van Hartingsveldt W., van Zeijl C.M.J., Harteveld G.M.,
RA Gouka R.J., Suijkerbuijk M.B.G., Luiten R.G.M., van Paridon P.A.,
RA Sellen G.C.X., Veenstra A.E., van Gorcom R.F.M.,
RA van den Hondel C.A.M.J.C.;
RA "Cloning, characterization and overexpression of the phytase-encoding
RT gene (phyA) of Aspergillus niger.";
RL Gene 127:87-94(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Mullaney E.J.;
RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 24-464.
RC STRAIN=NRRL 3135 / VAN TIEGHEM / FICUUM;
RX MEDLINE=93249451; PubMed=8397289;
RA Ullah A.H.J., Cummings B.J., Dischinger H.C. Jr.;
RA "Aspergillus ficuum phytase: complete primary structure elucidation
RT by chemical sequencing.";
RL Biochem. Biophys. Res. Commun. 192:747-753(1993).
RN [4]
RP SEQUENCE OF 71-93.
RC STRAIN=NRRL 3135 / VAN TIEGHEM / FICUUM;
RX MEDLINE=91298982; PubMed=1648914;
RA Ullah A.H.J., Cummings B.J., Dischinger H.C. Jr.;
RA "Cyclohexanediol modification of arginine at the active site of
RT Aspergillus ficuum phytase.";
RL Biochem. Biophys. Res. Commun. 178:45-53(1991).
RN [5]
RP CHARACTERIZATION, AND PARTIAL SEQUENCE.
RC STRAIN=NRRL 3135 / VAN TIEGHEM / FICUUM;
RX MEDLINE=89160685; PubMed=2852807;
RA Ullah A.H.J.;
RA "Aspergillus ficuum phytase: partial primary structure, substrate
RT selectivity, and kinetic characterization.";
RL Prep. Biochem. 18:459-471(1988).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).

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34 98 4.2 526 1 CLOS_CLOHI
35 98 4.2 1374 1 YODI_SCHPO
36 97.5 4.2 596 1 MPIP_SCHPO
37 97 4.2 822 1 YJF1_YEAST
38 96.5 4.1 504 1 C34_MOUSE
39 96.5 4.1 702 1 LYTS_STRR6
40 96.3 4.1 1419 1 ALAI_CANAL
41 96 4.1 2258 1 PAS_FIG
42 96 4.1 3137 1 CA36_CHICK
43 95.5 4.1 1328 1 YMT5_YEAST
44 95 4.1 3010 1 POLG_HCVJT
45 94.5 4.0 636 1 VNR6_YEAST

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P09870 clostridium
Q09884 schizosacch
P06652 schizosacch
P47046 saccharomyc
Q9jma7 mus musculu
P59206 streptococc
O13168 candida alb
Q99151 sus. scrofa
P15989 gallus gall
Q04214 saccharomyc
Q00269 h genome po
P53882 saccharomyc

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RC STRAIN=NRRL 3135 / VAN TIEGHEM / FICUUM;
 RX MEDLINE=97307250; PubMed=9764457;
 RA Kostrewa D., Gruninger-Leitch F., D'Arcy A., Broger C., Mitchell C.,
 RA van Loon A.P.;
 RI "Crystal structure of phytase from *Aspergillus ficuum* at 2.5-A
 RI resolution.";
 RJ Nat. Struct. Biol. 4:185-190(1997).
 CC -!- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
 CC FROM PHYTATE.
 CC -!- CATALYTIC ACTIVITY: Myo-inositol hexakisphosphate + H(2)O = 1D-
 CC myo-inositol 1,2,4,5,6-pentakisphosphate + phosphate.
 CC -!- BIOTECHNOLOGY: Is used as a food and feed additive. It can
 CC facilitate the degradation of phytin in soybean and other seeds
 CC used as food for monogastric animals. Sold by Novo Nordisk under
 CC the name Phytase Novo.
 CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; Z16414; CAA78904.1; -;
 CC EMBL; M94550; AAA32705.1; -;
 CC PIR; JN0656; CNO656.
 CC PDB; 1IHP; 18-MAR-98.
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 DR Pfam; PF00328; acid_phosphatase.
 DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
 DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 2.
 KW Hydrolase; Glycoprotein; Signal; 3D-structure.
 FT SIGNAL 1 23
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 FT ACT_SITE 82 82 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
 FT ACT_SITE 361 361 PROTON DONOR (BY SIMILARITY).
 FT DISULFID 31 40
 FT DISULFID 71 44
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 FT DISULFID 264 282
 FT DISULFID 436 444
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 FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .).
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 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .).
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 FT TURN 458 461
 FT HELIX 462 465
 FT TURN 466 467
 SQ SEQUENCE 467 AA; 51086 MW; 88FE9F3584341D6D CRC64;
 Query Watch 100.0%; Score 2334; DB 1; Length 467;
 Best Local Similarity 100.0%; Pred. No 5.4e-169; Indels 0; Gaps 0;
 Matches 444; Conservative 0; Mismatches 0;
 1 ASRNQSSCTVQGYQCFSETSH:WGOYAPFFESLANESVISPEVPACRVTFAOVLSRHG 60
 24 ASRNQSSCTVQGYQCFSETSH:WGOYAPFFESLANESVISPEVPACRVTFAOVLSRHG 83
 61 ARYPTSGKGYKYSALIEELIQONATTGKYAPLKYNYSLGADDLTFEGECLVNSGKIF 120
 84 ARYPTSGKGYKYSALIEELIQONATTGKYAPLKYNYSLGADDLTFEGECLVNSGKIF 143
 121 YQRYESLTRNIVPTFRSSSSSRVSIASGKKF:EGFQSTKLKDPRAQPGQSSPKIDWVISEA 180
 144 YQRYESLTRNIVPTFRSSSSSRVSIASGKKF:EGFQSTKLKDPRAQPGQSSPKIDWVISEA 203
 181 SSSNNTLDFGCTTFPDSSELADTVKAMPTATFVPSIRQRIENDLSGVTLLDTTEVTYMDM 240
 204 SSSNNTLDFGCTTFPDSSELADTVKAMPTATFVPSIRQRIENDLSGVTLLDTTEVTYMDM 263
 241 CSFDTISTSTVDTKLSRFDCLPETHDEWINDYLOS:KKYKHGAGNP:GFTQGVGVADEL 300
 264 CSFDTISTSTVDTKLSRFDCLPETHDEWINDYLOS:KKYKHGAGNP:GFTQGVGVADEL 323
 301 IARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLST 360
 324 IARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLST 383

QY 361 TTVENITOTDGFSSANTVPFASRLVYVEMQCAEQEPLRVLVNDRVPLHGCPCVALGR 420
 DB 384 TTVENITOTDGFSSANTVPFASRLVYVEMQCAEQEPLRVLVNDRVPLHGCPCVALGR 443
 QY 421 CTRDSFVRGLSFARSGGDWAECEFA 444
 DB 444 CTRDSFVRGLSFARSGGDWAECEFA 467

RESULT 2
 ID PHVA ASPAW STANDARD; PRT; 457 AA.
 AC P34753; 1994 (Rel. 28, Created:
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 3-phytase A precursor (EC 3.1.3.8) (Myo-inositol-hexaphosphate
 DE 3-phosphohydrolase A) (3 phytase A) (Myo-inositol hexakisphosphate
 DE phosphohydrolase A).
 GN PHVA OR PHV.
 OS Aspergillus awamori.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eutectiales; Trichocomaceae; Mitosporic Trichocomaceae; Aspergillus.
 CX NCBI_TaxID=105351;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AUK0243;
 RX MEDLINE=94040796; PubMed=8224894;
 RA Piddington C.S., Houston C.S., Palohelmo M.T., Cantrell M.A.,
 RA Mettinen-Oinonen A., Nevalainen H., Rambosk J.A.;
 RT "The cloning and sequencing of the genes encoding phytase (phy) and
 RT pH 2.5-optimum acid phosphatase (aph) from Aspergillus niger var.
 RT awamori";
 RL Gene 133:55-62(1993).
 CC -1- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
 FROM PHYTATE.
 CC -1- CATALYTIC ACTIVITY: Myo-inositol hexakisphosphate + H(2)O = ID-
 CC MYO-INOSITOL 1,2,4,5,6-pentakisphosphate + phosphate.
 CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.

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 or send an email to license@sib-sib.ch).

EMBL: J02421; AAA16898.1; ..
 PIR: JN0889; JN0889.
 HSP: P34752; 11HP.
 InterPro: IPR000560; HisAc_phosphatase.
 DR Pfam: PF0328; acid_phosphat; 1.
 DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.
 DR PROSITE: PS04778; HIS_ACID_PHOSPHAT_2; 1.
 KW Hydrolase; Glycoprotein; Signal..

FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 467
 FT ACT_SITE 82
 FT ACT_SITE 361 361 PROTON DONOR (BY SIMILARITY);
 FT DISULFID 31 40 BY SIMILARITY.
 FT DISULFID 7 414 BY SIMILARITY.
 FT DISULFID 215 465 BY SIMILARITY.
 FT DISULFID 264 282 BY SIMILARITY.
 FT DISULFID 436 444 BY SIMILARITY.
 FT CARBOHYD 27 27 N-LINKED (GLCNAC...) (POTENTIAL);
 FT CARBOHYD 59 59 N-LINKED (GLCNAC...) (POTENTIAL);
 FT CARBOHYD 105 105 N-LINKED (GLCNAC...) (POTENTIAL);
 FT CARBOHYD 120 120 N-LINKED (GLCNAC...) (POTENTIAL);
 FT CARBOHYD 207 207 N-LINKED (GLCNAC...) (POTENTIAL);
 FT CARBOHYD 230 230 N-LINKED (GLCNAC...) (POTENTIAL);
 FT CARBOHYD 339 339 N-LINKED (GLCNAC...) (POTENTIAL);
 FT CARBOHYD 352 352 N-LINKED (GLCNAC...) (POTENTIAL);

FT CARBOHYD 376 376 N-LINKED (GLCNAC...) (POTENTIAL);
 FT CARBOHYD 388 388 N-LINKED (GLCNAC...) (POTENTIAL);
 SC SEQUENCE 467 AA; 51275 MW; 118E828A5D7EC661 CRC64;

Query Match 98.1%; Score 2290; DB 1; Length 467;
 Best Local Similarity 97.3%; Pred. No. 110-165;
 Matches 432; Conservative 8; Mismatches 4; Indels C; Gaps 0;

QY 1 ASRNQSCDTVDQYQCFSETSHLWGQVAPFESLANESVSPVYAGCRVTFAQVLSRHG 60
 DB 24 ASRNQSCDTVDQYQCFSETSHLWGQVAPFESLANESA-SPQVYAGCRVTFAQVLSRHG 83
 QY 61 ARYFTDSKKKYSALIEIQONATTECKYAPLTYNYSLGADDLTPGEGELVNSGKIF 120
 DB 34 ARYFTESKKKYSALIEIQONATTECKYAPLTYNYSLGADDLTPGEGELVNSGKIF 143
 QY 121 YCRVESLTRNVPFRRSSGSRVVIASGKKFIEGQSTKLDKPRAPQGSSPKIDWVISEA 180
 DB 144 YCRVESLTRNVPFRRSSGSRVVIASGKKFIEGQSTKLDKPRAPQGSSPKIDWVISEA 203
 QY 181 SSSNNLDPGTCTVPEDSELADTVENAFATFVPSIRQRLNDLGGVTLTDTETVYLMDM 240
 DB 204 SSSNNLDPGTCTVPEDSELADTVENAFATFVPSIRQRLNDLGGVTLTDTETVYLMDM 263
 QY 241 CSFDTISTVDKILSPFCDLFTHDEMINDYLOSLKKYVGHGAGNPLGPGQGVYANEL 300
 DB 264 CSFDTISTVDKILSPFCDLFTHDEMINDYLOSLKKYVGHGAGNPLGPGQGVYANEL 323
 QY 301 IARLTHSPVHDTSSTNHTLDSPPATFPLNSTYADFSHDNGIISILFALGLYNGTKP-ST 360
 DB 324 IARLTHSPVHDTSSTNHTLDSPPATFPLNSTYADFSHDNGIISILFALGLYNGTKP-ST 363
 QY 361 TTVENITOTDGFSSANTVPFASRLVYVEMQCAEQEPLRVLVNDRVPLHGCPCVALGR 420
 DB 384 TTVENITOTDGFSSANTVPFASRLVYVEMQCAEQEPLRVLVNDRVPLHGCPCVALGR 443
 QY 421 CTRDSFVRGLSFARSGGDWAECEFA 444
 DB 444 CTRDSFVRGLSFARSGGDWAECEFA 467

RESULT 3
 ID PHYB EMENI STANDARD; PRT; 463 AA.
 AC OC0093;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 3-phytase B precursor (EC 3.1.3.8) (Myo-inositol-hexaphosphate
 DE 3-phosphohydrolase B) (3 phytase B) (Myo-inositol hexakisphosphate
 DE phosphohydrolase B).
 OS Emericella nidulans (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eutectiales; Trichocomaceae; Emericella.
 CX NCBI_TaxID=162425;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98067872; PubMed=9349716;
 RA Pasamonis L., Haiker M., Henriquez-Huecas M., Mitchell D.B.,
 RA van Loon A.P.;
 RT "Cloning of the phytases from Emericella nidulans and the
 RT thermophilic fungus Talaromyces thermophilus";
 RL Biochim. Biophys. Acta 1353:217-223(1997).
 CC -1- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
 FROM PHYTATE.
 CC -1- CATALYTIC ACTIVITY: Myo-inositol hexakisphosphate + H(2)O = ID-
 CC MYO-INOSITOL 1,2,4,5,6-pentakisphosphate + phosphate.
 CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.

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 CC -----

DR ENBL: US9803; AAB3687; 1; --
 DR HSSP; P34752; 1IHP.
 DR InterPro: IPR00056C; HisAc.phosphatase.
 DR Pfam: PF00328; acid phosphatase; 1.
 DR PROSITE: PS00616; HIS-ACID-PROSPHAT-1; 1.
 DR PROSITE: PS00778; HIS-ACID-PROSPHAT-2; 1.
 KM Hydroxylase; Glycoprotein; Signal.
 FT SIGNAL 1 19 POTENTIAL..
 FT CHAIN 20 463 3-PHYTASE B.
 FT ACT_SITE 80 80 REQUIRED FOR BINDING SUBSTRATE
 FT ACT_SITE 81 80 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
 FT ACT_SITE 357 357 PROTON DONOR (BY SIMILARITY).
 FT CARBOHYD 26 26 N-LINKED (GLCNAC..) (POTENTIAL).
 FT CARBOHYD 41 41 N-LINKED (GLCNAC..) (POTENTIAL).
 FT CARBOHYD 103 103 N-LINKED (GLCNAC..) (POTENTIAL).
 FT CARBOHYD 118 118 N-LINKED (GLCNAC..) (POTENTIAL).
 FT CARBOHYD 203 203 N-LINKED (GLCNAC..) (POTENTIAL).
 FT CARBOHYD 226 226 N-LINKED (GLCNAC..) (POTENTIAL).
 FT CARBOHYD 331 331 N-LINKED (GLCNAC..) (POTENTIAL).
 FT CARBOHYD 335 335 N-LINKED (GLCNAC..) (POTENTIAL).
 FT CARBOHYD 372 372 N-LINKED (GLCNAC..) (POTENTIAL).
 FT CARBOHYD 463 463 N-LINKED (GLCNAC..) (POTENTIAL).
 SC SEQUENCE 463 AA; 5:786 MW; ECC5827D1E1C92A2 CRC64;

Query Match 65.7%; Score 1532.5; DB 1; Length 463;
 Best Local Similarity 63.8%; Pred. No. 2; e-108;
 Matches 279; Conservative 69; Mismatches 86; Indels 3; Gaps 2;

QY 7 SCOTVQGVQCFSETHLWQVAPFSLANESVISPEVAGCRVTFQVLSRHGARYPTD 66
 DB 28 SNTAGGGVQCFENSHVAGVQSPFESIQESAISEDVPHGCEVTFQVLSRHGARYPTD 87
 QY 67 SKGKYSALIEEIQONATFDGKYAFJKTNYNSLGADLTPGEOELVNSGICKFYQYES 126
 DB 88 SKSKAYSGLIEAQKATSFQWGYAFLESYNTLGADDLTFSEQVMSGAKFYARYKN 147
 QY 127 LTRNIVPFRSSGSSRVIASGKAFIEGPOSTKLKDFRAGQGGSSPKIDVYSEASSSNT 186
 DB 148 LARKNTFPFRASGSDRVASAEKFNIGFRKALDHGSK--RATVAVNVTFEIDGFNT 205
 QY 187 LDPGCTVVEDSELAQTVGKFTATV6SIRIENDLSGVLTCTEVTYNDMSSEPTI 246
 DB 206 LCHSTCVSENDERADEIEANFPALMGPPRKLENDLPGLKLTENVYLYMDKSPFTM 265
 QY 247 STSTVDTKLSPFCGLPHEWYNYQLQSLKKYHGAGNPLSPFGVGYAVELLARVTH 306
 DB 266 ARTAHGTSLSPFCAIFTEREKLYDYLQSLSKYGYGAGSPJGPAQGIQFNELIARLTQ 325
 QY 307 SPVEDDTSSNHTDSSPATFELNSTLYADPSHDNGIISILFALGYNGTKPSTTTVENI 366
 DB 326 SPVDNTSINHLLDSAPATFPLDRKLYADPSHDNSWISIFFANGLYNGTQPLSDVSESI 385
 QY 367 TQDGESSAMTVFASRLYVMMQCAQEPVVRVLDNRVNVPLRGCPVDALGRCTRDSF 426
 DB 386 QENDGYAASWTVPFGARAYFELMQCE-KKEPLVRVLNDRVNVPLRGCAVQKRGRTILDQW 444
 QY 427 VRGLSFARSGGVWAEFCF 443
 DB 445 VEGINFARSGGNKTKCF 461

RESULT 4

PPA3_YEAST STANDARD; PRT; 467 AA.
 AC P24031;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Constitutive acid phosphatase precursor (EC 3.1.3.2).

GN PH03 CR YBR092C CR YBR0813.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes.
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85037940; PubMed=6093051;
 RA Bajwa W., Mewhach B., Rudolph H., Schweingruber A.-M., Hinnen A.;
 RT "Structural analysis of the two tandemly repeated acid phosphatase
 genes in yeast";
 RC Nucleic Acids Res. 22:7721-7739(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95208357; PubMed=7900426;
 RA Mannhaupt G., Stucka R., Ehme S., Vetter I., Feldmann H.;
 RT Analysis of a 70 kb region on the right arm of yeast chromosome II";
 RL Yeast 10:1363-1381(1994).
 CC -1- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
 alcohol + phosphate.
 CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
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 or send an email to license@isb-sib.ch).
 CC -----
 DR ENBL: X01C80; CAA25557.1;
 DR ENBL: X78993; CAA55597.1;
 DR EMBL: Z35961; CAA85045.2;
 DR PIR: S48259; PABYCC.
 DR HSSP; P34755; 1QFX.
 DR SGD; S0C30287; Ciperiplasmic space (sensu Fungi); IMP.
 DR GO: GO:0030287; Ciperiplasmic space (sensu Fungi); IMP.
 DR GO: GO:0030993; F1 acid phosphatase activity; IMP.
 DR GO: GO:0018882; P1 thiamin transport; IMP.
 DR InterPro: IPR000560; HisAc.phosphatase.
 DR Pfam: PF00328; acid phosphatase; 1.
 DR PROSITE: PS00616; HIS-ACID-PROSPHAT-1; 1.
 DR PROSITE: PS00778; HIS-ACID-PROSPHAT-2; 1.
 KM Hydroxylase; Glycoprotein; Signal; Multi-gene family.
 FT SIGNAL 1 2 POTENTIAL..
 FT CHAIN 18 467 CONSTITUTIVE ACID PHOSPHATASE.
 FT ACT_SITE 75 75 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
 FT ACT_SITE 337 337 PROTON DONOR (BY SIMILARITY).
 FT CARBOHYD 97 97 N-LINKED (GLCNAC..) (POTENTIAL).
 FT CARBOHYD 103 103 N-LINKED (GLCNAC..) (POTENTIAL).
 FT CARBOHYD 162 162 N-LINKED (GLCNAC..) (POTENTIAL).
 FT CARBOHYD 192 192 N-LINKED (GLCNAC..) (POTENTIAL).
 FT CARBOHYD 250 250 N-LINKED (GLCNAC..) (POTENTIAL).
 FT CARBOHYD 315 315 N-LINKED (GLCNAC..) (POTENTIAL).
 FT CARBOHYD 356 356 N-LINKED (GLCNAC..) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC..) (POTENTIAL).
 FT CARBOHYD 439 439 N-LINKED (GLCNAC..) (POTENTIAL).
 FT CARBOHYD 445 445 N-LINKED (GLCNAC..) (POTENTIAL).
 FT CARBOHYD 456 456 N-LINKED (GLCNAC..) (POTENTIAL).
 FT CARBOHYD 461 461 N-LINKED (GLCNAC..) (POTENTIAL).
 FT CONFLICT 219 221 DED -> MKT (IN REF. 1).
 SQ SEQUENCE 467 AA; 52776 MW; 05FBB80DEB41B0FF CRC64;

Query Match 16.5%; Score 385; DB 1; Length 467;

Best Local Similarity 26.1%; Pred. No. 1; e-21;

Matches 113; Conservative 63; Mismatches 195; Indels 62; Gaps 22;

QY 26 GOYAPFFSLANESVISPEVAGCRVTFQVLSRHGARYPTD SKGKYSALIEEIQONAT 85

DB 42 GAGAGPVSPFGDYGISRLDPEGCENKQLQMLARHGERVPTYSKGTATMKTWKLSNTRYQ 101

QY 86 FQGYAFLK-TNYSLGADD-----LTPF-GEOELVNSGICKFYQYESLTR 129

```
Db 102 FNGSLFNDYFFRRDDCELEMTTFANSDVNLAPYTGEMAKHAREFLACYGYE 161
Qy 130 NIVPFF-IRSSGSRVIAAGKKFIEGPOSTKLKDPRAQPGSSPKIDVISEASSNNTLD 188
Db 162 NOTSFPIFAASSRVRHDTAQYFDIG-----LGD-----QFN:SLQTVSEAMGANTLS 210
Qy 189 PGCTVFEDSELADTVENATATFVPSIRGLJENLDSGVTLTDTETVYLMQMCSEDTIST 246
Db 211 AGNACFGWDEADNDILCKYDTTYLDDIARLKNENKGLNLTSCDANTLPAWCAYSKAR 270
Qy 249 STYDTKLSPPCCJLTHDEWINYDYLSKKYVGHGAGNPLGPQGVGYANELLARLTHSP 306
Db 271 GYSDV-----CDITTEDELYRYSGQDLVSFYQDGPYGMIRSVGANLENNT-KLLKQSE 325
Qy 309 VHDOTSSNHTLDSSEATFPLNSLYADFSNDNIIISILFALG:YNGTKPLSTTTVENITC 368
Db 326 TDD-----LKVMSFTHTCTDLNLYVLTAGTIDCKNLTABYVFPNGN 367
Qy 369 TDGFSANWYPPASRLVYVEMNOCAGDEPLVRV:VNDERVVELHGCPDVALGRCTRFSF-- 476
Db 369 T--FHKSYYVPOGARVYTERFQC--SNQTVRVVINDAVVETCTSGPGFSCENIDFYD 423
Qy 427 -----VRGLSFAR 434
Db 424 YAEKRVAGTDFLK 436

RESULT 5
PPAS YEAST
ID PPAS YEAST STANDARD; PRT: 457 AA.
AC P00635;
DT 21-JUL-1986 (Ref. 31, Created)
DT 01-OCT-1994 (Ref. 30, Last sequence update)
DE Repressible acid phosphatase precursor (EC 3.1.3.2) (P60).
GN PHOS OR YBR031C OR YBR0814.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
CX NCBI_taxID=4932;
RN SEQUENCE FROM N.A., AND SEQUENCE OF 18-26.
RP MEDLINE=83168913; PubMed=6100772;
RA Arima K., Oshima T., Kubota I., Nakamura N., Mizunaga T., Toh-E A.;
RT "The nucleotide sequence of the yeast PHOS gene: a putative precursor
of repressible acid phosphatase contains a signal peptide.";
RJ Nucleic Acids Res. 11:1657-1672(1983).
RN (2)
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-45.
RX MEDLINE=85037940; PubMed=6093051;
RA Bajwa W., Meyhack B., Rudolph H., Schweingruber A.-M., Hinner A.;
RT "Structural analysis of the two tandemly repeated acid phosphatase
genes in yeast.";
RJ Nucleic Acids Res. 12:7721-7739(1984).
RN (3)
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=95208357; PubMed=7900426;
RA Mannhaupt G., Stucka R., Ehle S., Vetter T., Feldmann H.;
RT "Analysis of a 70 kb region on the right arm of yeast chromosome II.";
RJ Yeast 10:1363-1381(1994).
RN (4)
RP SEQUENCE OF 1-44 FROM N.A.
RX MEDLINE=87064474; PubMed=3537710;
RA Tait-Kamradt A.G., Turner K.J., Kramer R.A., Elliott O.C.,
RA Bostian S.J., Thill G.P., Rogers D.T., Bostian K.A.;
RT "Reciprocal regulation of the tandemly duplicated PHOS/PHO3 gene
cluster within the acid phosphatase multigene family of Saccharomyces
cerevisiae.";
RJ Mol. Cell. Biol. 6:1855-1865(1986).
CC -!- CATALYTIC ACTIVITY: An orthophosphoric monester + H(2)O = an
alcohol + phosphate.
```

```
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- INDUCTION: REPRRESSED BY INORGANIC PHOSPHATE.
CC -!- PTM: GLYCOSYLATED DURING SECRETION ACROSS THE MEMBRANE.
CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC -----
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CC -----
Db EMBL: W01320; CAA24630.1; .
Db EMBL: X01079; CAA25555.1; .
Db EMBL: X78993; CAA55598.1; .
Db EMBL: X35962; CAA85046.1; .
Db EMBL: X01080; CAA25556.1; .
Db FIR: S05795; PABYC.
Db HSSP: P34755; IQFX.
Db SGD: S000297; PHOS.
Db GC: G00009277; Cereal wall (sensu Fungi); IDA.
Db GC: G00030287; C:periplasmic space (sensu Fungi); NAS.
Db InterPro: IPR000560; HisAc_Phasphatase.
Db Pfam: PF00328; acid_phosphat_1.
Db PROSITE: PS00616; HIS-ACID-PHOSPHAT-1; 1.
Db PROSITE: PS00778; HIS-ACID-PHOSPHAT-2; 1.
KW Hydroxase; Glycoprotein; Signal; Multigene family.
FT SIGNAL 1..17
FT CHAIN 18..467
FT ACT_SITE 75..75
FT ACT_SITE 337..337
FT CARBOHYD 97..97
FT CARBOHYD 103..103
FT CARBOHYD 162..162
FT CARBOHYD 192..192
FT CARBOHYD 250..250
FT CARBOHYD 315..315
FT CARBOHYD 356..356
FT CARBOHYD 390..390
FT CARBOHYD 439..439
FT CARBOHYD 445..445
FT CARBOHYD 456..456
FT CARBOHYD 461..461
FT CONFLICT 36..36
FT CONFLICT 130..130
FT CONFLICT 294..294
FT CONFLICT 446..446
FT CONFLICT 462..462
FT CONFLICT 466..466
SQ SEQUENCE 467 AA; 52858 MW; DC3C9504BC2D3DC CRC64;

Query Match 16.5%; Score 385; DB 1; Length: 467;
Best Local Similarity 26.2%; Pred. No. 1.2e-21;
Matches 114; Conservative 66; Mismatches 189; Indels 66; Gaps 14;

Qy 26 GOVAPFESLANESVISPACRVTFQAQLSRHGRVYFTDSKGYKYSALIEIQONATT 85
Db 42 GGAGPYISFGDYG-SRDLPECEKQLQMGVHGRYPTVSLAKTISKTWKLSNYTRQ 101
Qy 86 FQGYAFLEK-TYNYSIGADD-----LTPF-GEQELVNSGKIFQRYESLTR 129
Db 102 FNGSLFNDYFFRRDDDDLEMETTFANSDVNLAPYTGEMAKHAREFLACYGYE 161
Qy 130 NIVPFF-IRSSGSRVIAAGKKFIEGPOSTKLKDPRAQPGSSPKIDVISEASSNNTLD 188
Db 162 NOTSFPIFAASSRVRHDTAQYFDIG-----LGD-----QFN:SLQTVSEAMGANTLS 210
Qy 189 PGCTVFEDSELADTVENATATFVPSIRGLJENLDSGVTLTDTETVYLMQMCSEDTIST 247
Db 211 AGNACFGWDEADNDILCKYDTTYLDDIARLKNENKGLNLTSCDANTLPAWCAYSKAR 266
Qy 249 STYDTKLSPPCCJLTHDEWINYDYLSKKYVGHGAGNPLGPQGVGYANELLARLTHSP 306
```

Db 267 ---VNAKGVSDVCDIFTKDELVHYSVYQDLHYYHGGPYD::KSVGSLNLFNASXKLLXQ 323
 QY 307 SPVHDTSSNHTLSSSPATFFPLNSTLYARDFSHNGIISILFALGLYNTKPLSTTTVENI 366
 Db 324 SE:QC-----QKWLSTHTDIDILNFTAG::DDKNLTAAYVYVPM 365
 QY 367 TOTDGFSSANTVFFASRLVVMQCAOEPLVRLVNDVVPLKGPVDAIGRCRDSF 426
 Db 366 GNT--PHRSNYVQGARVYTERFQC--SNDTVRVVINDAVVFIETCSTGGFSCSE:NDP 421
 QY 427 -----VRGLSPAR 434
 Db 422 YDVAEKRVAGTDZLK 436

RESULT 6

PPAD_YEAST STANDARD; PRT; 468 AA.
 AC P52290;
 DT 01-OCT-1996 (Rel. 34, Created;
 DT 01-OCT-1996 (Rel. 34, Last sequence update;
 DT 15-JUL-1993 (Rel. 38, Last annotation update;
 DE Probable acid phosphatase YD024C precursor (EC 3.1.3.2).
 GN YD024C OR D2815.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
 CC alcohol + phosphate.
 CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 CC
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 CC
 CC EXBL; Z48432; CAA88335.1; -;
 CC EXBL; Z74072; CAA98583.1; -;
 CC PIR; S52495; S52495.
 CC HSSP; P34755; 1QFX.
 CC SGD; S0002132; YD024C.
 CC GO; GO:0007125; P:invasive growth; IGI.
 CC GO; GO:0007124; P:pseudohyphal growth; IMP.
 CC InterPro; IPR030560; HisAc_Phasptase.
 CC Pfam; PF00328; acid phosphat; 1.
 CC PROSITE; PS00616; HIS ACID PHOSPHAT 1; 1.
 CC PROSITE; PS00778; HIS ACID PHOSPHAT 2; 1.
 CC Hydrolase; Glycoprotein; Signal; Multigene family.
 CC FT SIGNAL 20 BY SIMILARITY.
 CC FT CHAIN 21 468 PROBABLE ACID PHOSPHATASE YD024C.
 CC FT ACT_SITE 76 76 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
 CC FT ACT_SITE 338 338 PROTON DONOR (BY SIMILARITY).
 CC FT CARBOHYD 98 98 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD 163 163 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD 193 193 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD 202 202 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD 238 238 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD 251 251 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD 316 316 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD 357 357 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD 391 391 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD 457 457 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD 462 462 N-LINKED (GLCNAC...) (POTENTIAL).

SQ SEQUENCE 468 AA; 53076 MW; 1F07FF374DDF:62C CRC64;
 Query Match 15.8%; Score 368; DB :; Length 468;
 Best local similarity 25.0%; Pred. No. 2.3e-20;
 Matches 109; Conservative 74; Mismatches 181; Indels 72; Gaps 13;
 QY 26 GOVAPFESLANESVPEFACGRVTFQAQLSRGARYPTDSKGGKYSALIEE:QCNATT 85
 Db 43 GSAPIFESFANYGIPTDIPGCRLTQVM:GRHGRYFTRSEAKC:FEVWYK:SNYTKG 102
 QY 86 FDKYAFALKT:YNYSJ-----GADLTPF-GECELVNSGKIFYQYVESLTPR 129
 Db 103 YEGSLSLNNGYEFTFPDESLL:EMETT:QNSIDVLNPLYTGEYNARHAREFLARYKLMY 162
 QY 130 N:VFP-IRSSGSSRVIAAGKPE:---GFGSTKLKOPRAQPGGSSPKIDVIVSEASSN 184
 Db 163 NCTNPFITTNKRIYDTAQYPAEALGGGNIS-----LQTSNSSSGA 207
 QY 185 NTLDPOTCTVFEDSELAOTVEANFTATFVPS:RQSLNDLSGVTLTDT:EVTYLMDXGSPD 244
 Db 208 N:LAAKSCPMNNSNANDILWYSRSDYLENISDRLENDKGLNLSRDAALF:SWCAFE 267
 QY 245 T:STSTVDTK-LSPKCDL:FTHDEW:NYDYLQSLKKYVGHGAGNPLGPTQGVGYANELIAR 303
 Db 268 -----LNAGYSNICDIPSAELIHYSYETDLSFYQNGPGYKLIKSIGANLFRATV-K 320
 QY 304 LTHSPVHDDTSSNHTLSSSPATFFPLNSTLYARDFSHNGIISILFALGLYNTKPLSTTTV 363
 Db 321 LIRQSAH-----LDQKWLSTHTDIDILNFTAGLIDDTNRLT:NHV 363
 QY 364 EN:TOTDGFSSANTVFFASRLVVMQCAOEPLVRLVNDVVPLKGPVDAIGRCRTR 423
 Db 364 P--FRDHSYHRSY:PGGARVYTERFQC--SNDSYRVVINDAVVFIETCSTGGFSCSE 419
 QY 424 DSP-----VRGLSPF 432
 Db 420 GFYEYAKDLRGVSP 435

RESULT 7

PPAD_YEAST STANDARD; PRT; 467 AA.
 AC P55842;
 DT 01-JUN-1994 (Rel. 29, Created;
 DT 01-JUN-1994 (Rel. 29, Last sequence update;
 DT 01-NOV-1997 (Rel. 35, Last annotation update;
 DE Acid phosphatase PHO1 precursor (EC 3.1.3.2) (P56).
 GN PHO1 OR YAR071W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RC MEDLINE=95249563; PubMed=7731988;
 RA Bussey H., Kaback D.B., Zhong W., Vo D.T., Clark M.W., Fortin N.,
 RA Hall J., Quellet B.F.P., Keng T., Barton A.B., Su Y., Davies C.K.,
 RA Storms A.K.;
 RA "The nucleotide sequence of chromosome I from Saccharomyces
 RA cerevisiae";
 RA Proc. Natl. Acad. Sci. U.S.A. 92:3809-3813(1995).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC Chen J.Y., Gong Y.I., Ao S.Z.;
 CC "The primary structure of acid phosphatase gene PHO1 in S.
 CC cerevisiae and comparison with other gene families";
 CC Acta Biochim. Biophys. Sin. 21:437-444(1989).
 CC -1- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
 CC alcohol + phosphate
 CC -1- INDUCTION: S.CEREVISIAE HAS 2 TYPES OF ACID PHOSPHATASE: ONE IS
 CC CONSTITUTIVE AND THE OTHER IS REPRESSIBLE BY INORGANIC PHOSPHATE.
 CC -1- PTM: GLYCOSYLATED DURING SECRETION ACROSS THE MEMBRANE.

CC -- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.

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CC

DR EMBL: L28920; AAC03508.1; ..

DR EMBL: U19789; AAA73479.1; ..

DR PIR: S53476; S53476.

DR HSSP: P34755; IQFX.

DR SGD: S0000094; PHO1.

DR GO: GO:0005576; C:extracellular; IDA.

DR GO: GO:0003993; F:acid phosphatase activity; IDA.

DR InterPro: IPR000560; HisAc_phsptase.

DR Pfam: PF00128; acid phosphatase 1

DR PROSITE: PS00616; HIS-ACID-PHOSPHAT_1; 1.

DR PROSITE: PS00778; HIS-ACID-PHOSPHAT_2; 1.

KW Hydroxylase; Glycoprotein; Signal; Multigene family.

FT SIGNAL 1 17

FT CHAIN 18 467

FT ACT_SITE 75 75

FT ACT_SITE 337 337

FT CARBOHYD 162 162

FT CARBOHYD 192 192

FT CARBOHYD 250 250

FT CARBOHYD 315 315

FT CARBOHYD 356 356

FT CARBOHYD 390 390

FT CARBOHYD 439 439

FT CARBOHYD 445 445

FT CARBOHYD 461 461

FT CONFLICT 17 17 A -> L (IN REF. 2).

FT CONFLICT 82 83 VS -> AR (IN REF. 2).

FT CONFLICT 150 150 R -> H (IN REF. 2).

FT CONFLICT 354 354 K -> Q (IN REF. 2).

FT CONFLICT 423 423 D -> G (IN REF. 2).

SQ SEQUENCE 467 AA; 52757 MW; AECDC1C946B326C3 CRC64;

Query March 15.18; Score 352; DB 1; Length 467;

Best Local Similarity 24.4%; Pred. No. 3.7e-19;

Matches 107; Conservative 70; Mismatches 189; Indels 72; Gaps 14;

QY 26 GQVAPFFSLANESVISPEVAGCRVTPAQVLSRHGARYPTDSKGGKYSALIEIQQVAT 85

DB 42 GSGPYVSPFGCYISRLPESCEMKQVMGRHGERVPTVSKAKSIMTWYKLSNVTGQ 101

QY 86 PDGYAFK-----TNYSL-----GADLTFF-GEQELVNSGKIFYORYESLJR 129

DB 102 FSGALSFENDYEFPIRDTKNLEMTTANSVNLNPTTGEMNAKHARDFLAQGYMVE 161

QY 130 NIVPF-IESGSSRVIASGKFFEGFQSTKLDPRAQPGSSPKIDV---VISEASSN- 184

DB 162 NQTSFAVFTSNRCHDTAQAFIDGL-----GKFNISLOTISEASAGA 256

QY 185 NTLRP-GLTCVFESLADTVEANFTATFVPSIFQRLENDLSGVTLTIDTETVLMDCSF 243

DB 207 NTLNAAHSCPAKDD-DVNDL-LKAYDKYLSG-AKRLNKENKGLNLTSSDAN-FFAKCAY 265

QY 244 DTISTVDTKLSFCDLFTDCEMINVDYLOSLLKKYYGHGAGNPLGTQGVGVANELIAR 303

DB 266 EINARG-----YSDICNIFTDELVRFSYGOLETYTGTGPGVWRSVGNK-FNASVKL 320

QY 304 LTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHDNGI-SILFALGLYNGTKELSTTV 363

DB 321 LKESVQD-----QKWLVSF-CHDTDLNLYLTIGI-DQXNKLTAHV 362

QY 364 ENIQTDGFSSAWTPFASRLYVEMMOCAQBEPLVRLVNDRVVPLHGGCPVDAIGCTR 423

DB 363 PPMENT--FHSRWYVPGQARYVTEKQC--SNDTVRVVINDAVVPIETCTGPGFSCFI 418

QY 424 DSF-----VRG-SFAR 434

DB 419 NDFDYDAEKRVAGTDFLK 436

RESULT 8

PPAC_YEAST STANDARD; PRT: 467 AA.

AC P38593;

DT 01-FEB-1995 (Rel. 31; Created;

DT 01-FEB-1995 (Rel. 31; Last sequence update)

DT 01-FEB-1995 (Rel. 31; Last annotation update)

DE Acid phosphatase PHO12 precursor (EC 3.1.3.2);

GN PHO12 OR YHR215W.

OS Saccharomyces cerevisiae (Baker's yeast).

CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI_TaxID=4932;

RR [1]

RF SEQUENCE FROM N.A.

RC STRAIN=S288c / AB972;

EX MEDLINE=94378003; PubMed=8991229;

RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,

RA Du Z., Favello A., Fulton J., Gattung S., Geisel C., Kirsten J.,

RA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,

RA Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser J.,

RA Nhan M., Rifkin J., Riles L., St Peter H., Trevisan E., Vaughan K.,

RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,

RA Vaudin M.

RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome

PT VII..";

RL Science 265:2077-2082(1994).

CC -- CATALYTIC ACTIVITY: An orthophosphoric monoester - H₂O = an

CC alcohol + phosphate.

CC -- INDUCTION: S-CEREVISIAE HAS 2 TYPES OF ACID PHOSPHATASE: ONE IS

CC CONSTITUTIVE AND THE OTHER IS REPRESSIBLE BY INORGANIC PHOSPHATE.

CC -- PTM: GLYCOSYLATED DURING SECRETION ACROSS THE MEMBRANE FAMILY.

CC -- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.

CC

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CC

DR EMBL: L00029; AAB69729.1; ..

DR PIR: S4896; S4896.

DR HSSP: P34755; IQFX.

DR SGD: S0001258; PHO12.

DR InterPro: IPR000560; HisAc_phsptase.

DR Pfam: PF00328; acid phosphatase 1.

DR PROSITE: PS00616; HIS-ACID-PHOSPHAT_1; 1.

DR PROSITE: PS00778; HIS-ACID-PHOSPHAT_2; 1.

KW Hydroxylase; Glycoprotein; Signal; Multigene family.

FT SIGNAL 1 17

FT CHAIN 18 467

FT ACT_SITE 75 75

FT ACT_SITE 337 337

FT CARBOHYD 162 162

FT CARBOHYD 192 192

FT CARBOHYD 250 250

FT CARBOHYD 315 315

FT CARBOHYD 356 356

FT CARBOHYD 390 390

FT CARBOHYD 439 439

FT CARBOHYD 445 445

FT CARBOHYD 461 461

SQ SEQUENCE 467 AA; 52699 MW; BEC6C6CDF39B845B CRC64;


```

Query Match      15.1%; Score 352; DB 1; Length 467;
Best Local Similarity 24.4%; Pred. No. 3,7e-19;
Matches 107; Conservative 7c; Mismatches 189; Indels 72; Gaps 14;

QY 26 GQYAPFFSLANESVISPEVPAGCRVTFPAQVLRHGRARYPTDSKKYKAL-EE-CQNAIT 35
DB 42 GSGGPVYSPGDYIGRDLFESCEMCKQVMWGRHGERVPTVSKASIVTTWKLSNYTGO 101
QY 86 FDKYAFLEK-----TYNVL-----GADDLTPP-GEQELVNSGKRYQYES:TR 129
DB 102 FSGALSFNLDDYEFFIRDKNLEMETELANSVNVLPYTGEMAKRHARDLFAQGYNVE 162
QY 130 NIVPFF-IRSSGSRV-ASGKKFIEGQSTKCKDPAQPOSSPKIDV---VISEASSN- 194
DB 162 NCTSPAVFTSNRCHDTAQQYFDGL-----CDKENISLCIISAESAGA 206
QY 185 NTLDP-GTCVFESELAOTVEANFTATVPISIRORLNDLSGVTLTDEVTYLMDMCSF 243
DB 207 NTLASHSFPAWD-DVNDLILKDYCTKYLSGIKAKLENKENGLNLTSSDANTFFAWCAY 265
QY 244 DT-STSTVORLSPFFCDLPHDEMIVDYLOS-KKYGHGAGNPLGPTQGVGYANEELAR 303
DB 266 EINARG-----YSDICNIFKDELVRPSYQDLE-VYQTGPQYDVVRSGANLENASVKL 320
QY 304 LTHSPVHDOTSSNHTLDSSEPATFPLNSTLYADPFSHNGIIS-LFALGLYNGTKPLSTTV 363
DB 321 LKSEVQD-----QKWLSTHTD-LNYLTGTIGIICDQNNLTAEHV 362
QY 364 ENITQDGFSSAMTVFPASRLVYVMCOCAOEPLVRLVNDRVVPLHGCQPDALGRCTR 423
DB 363 PFMENT--FHSRYVPCGARVTEKFC--SNQTVYRVINDAVVPIETCTGPGFSCET 418
QY 424 DSF-----VRGLSPAR 434
DB 419 NDFYGYAEKRVAGTDFELK 436

RESULT 9
PPAS_KULUA STANDARD; PRT; 469 AA.
AC P32289;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Repressible acid phosphatase precursor (EC 3.1.3.2).
GN P305.
OS Kluyveromyces lactis (Yeast).
CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
CC NCBI_TaxID=28985;
RN 1;
FP SEQUENCE FROM N.A.
RC STRAIN=CBS 2359/152;
RA Ferminan E.;
RJ Thesis (1995); University of Salamanca, Spain.
CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H2O = an
CC alcohol + phosphate.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- INDUCTION: REPRESSED BY INORGANIC PHOSPHATE (BY SIMILARITY).
CC -!- PM: GLYCOSYLATED DURING SECRETION ACROSS THE MEMBRANE.
CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; 233995; CAA83964.1; --
CC HSSP; P34755; 1QFX.

DR PPAS_KULUA
DR PROSITE; P50328; acid-phosphat; 1.
DR PROSITE; P50346; H-S-Acid-Phosphat; 1.
DR PROSITE; P50378; H-S-Acid-Phosphat; 1.
KW Hydroxylase; Glycoprotein; Signal; Multigene family.
FT SIGNAL 1 16
FT CHAIN 17 469
FT ACT_SITE 77 77 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
FT ACT_SITE 339 339 PROTON DONOR (BY SIMILARITY).
FT CARBOHYD 23 23 N-LINKED (GLCNAC).
FT CARBOHYD 31 31 N-LINKED (GLCNAC).
FT CARBOHYD 32 32 N-LINKED (GLCNAC).
FT CARBOHYD 129 129 N-LINKED (GLCNAC).
FT CARBOHYD 201 201 N-LINKED (GLCNAC).
FT CARBOHYD 229 229 N-LINKED (GLCNAC).
FT CARBOHYD 250 250 N-LINKED (GLCNAC).
FT CARBOHYD 317 317 N-LINKED (GLCNAC).
FT CARBOHYD 332 332 N-LINKED (GLCNAC).
FT CARBOHYD 447 447 N-LINKED (GLCNAC).
SQ SEQUENCE 469 AA; 52532 MW; 863B528D0740AA7E CRC64;

Query Match      15.0%; Score 351; DB 1; Length 469;
Best Local Similarity 24.8%; Pred. No. 4,5e-19;
Matches 119; Conservative 66; Mismatches 177; Indels 118; Gaps 17;

QY 12 DQGYQCF-----SETSLWQYAPFFSLANESVISPEVPAGCRVTFPAQVLSRHGR 62
DB 22 DNGTCYALNNSTTDESIFSLNQ-GPHYDYPQSFGIPVEVPDQCTVEHVQMLARHGR 80
QY 63 YETDSGKKYKYSALIEIQONATTDGKYAFUKTYNSLGGADLTFFGSOELVNSGIFQY 122
DB 91 YPTASRGLMIALMDKLKE----FQGY-----NDPLEVFNDFEYFVSNTKYFD 125
QY 123 R-----YESLRNIVPPIRSSGSSRVIASGKKFIEG 153
DB 126 QLTNSTEVDPSNPFYAGAKTAQHLGKYIAYNYGDLFSDSNPVFSS-SGRVHCTAKYVVS 184
QY 154 FOSTKLKDPRAOPGQSSPKIDV-----VISEASSN-NLIDPGTCTVFDESSLADTVAN 207
DB 165 LEE-----ELDQLDQ:IQENETSGANSLTPADSCMTYNGSLGDEYFEN 229
QY 208 FTAIVPPIRQ--LERULSGVTITDTETVYLMDCSFDITISTVTKLSPPFCDLTHD 265
DB 230 ATLPLYLTDIKNEMKKNSNLTLEHDDIELVDWCAFE:NVKGS-----SAYCDLEFN 284
QY 266 EMINDYLOSLLKYYCHGAGNPLGPTQGVGYANELIARLTHSPVHDOTSSNHTLDSSEAT 325
DB 285 DLVAKSYANVNNFYRGAGNPMNPISGVJNAYNKLTCQ------- 327
QY 326 FPLKSTLYADFSHNGIISILFALGLY-NGTKPLSTTV--ENITQDGFSSAMTVFPAS 382
DB 325 -ELDNKWLSPSHDTCQCFISALGLIDNGVTEYSLDQVDFONICOL-----SWTPNGS 381
QY 383 RLYVENMOCQAOEPLVRLVNDRVVPLHGCQPDALGRCTRQSF-----VRGLSPAR 435
DB 382 RIPTKLEK--GMASYRVYINDVPIPVGCTSGPGFSCPIEDFDQVITNRLNGIDYVS 439

RESULT 10
PPHY_ASFNG STANDARD; PRT; 479 AA.
AC P34754;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 3-phytase B precursor (EC 3.1.3.8) (Myo-inositol-hexaphosphate
DE 3-phosphohydrolase B) (3 phytase B) (Myo-inositol hexakisphosphate
DE phosphohydrolase B).
GN PPHYB.
OS Aspergillus niger.
CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
CC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
CC NCBI_TaxID=5061;

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RN [1]
R2 SEQUENCE FROM N.A., AND SEQUENCE OF 20-101; 133-141 AND 376-399.
RX MEDLINE=93371452; PubMed=7916610;
RA Brilich K.C., Montalbano B.G., Mullaney E.J., Dischinger H.C. Jr.,
RT Ullah A.H.J.;
RL "Identification and cloning of a second phytase gene (phyB) from
ASpergillus niger (ficusum)";
RL Biochem. Biophys. Res. Commun. 195:53-57(1993).
CC -1- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
FROM PHYTATE.
CC -2- CATALYTIC ACTIVITY: Myo-inositol hexakisphosphate + H2O = 1D-
myo-inositol; 1,2,4,5,6-pentakisphosphate + phosphate.
CC -3- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
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CC
EMBL: J20567; AAA0234; .
DR HSSP; P34755; 1QFX.
DR InterPro; IPR000560; HisAc phosphatase.
DR Pfam; PF00328; acid phosphatase.
DR PROSITE; PS00616; HIS-ACID-PROSPHAT_1; 1.
DR PROSITE; PS00778; HIS-ACID-PROSPHAT_2; 1.
KW Hydrolase; Glycoprotein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 479
FT ACT_SITE 81 81
FT ACT_SITE 82 82
FT ACT_SITE 337 337
FT CARBOHYD 106 106
FT CARBOHYD 191 191
FT CARBOHYD 227 227
FT CARBOHYD 250 250
FT CARBOHYD 315 315
FT CARBOHYD 425 425
FT CARBOHYD 442 442
FT CARBOHYD 458 458
FT SEQUENCE 479 AA; 536.1 MW; 39504DA2950FDFC4 CRC64;
Query Match 14.5%; Score 339.5; DB 1; Length 479;
Best Local Similarity 27.9%; Pred. No. 3.4e-18;
Matches 109; Conservative 60; Mismatches 165; Indels 57; Gaps 15;
QY 40 ISPEVAGCRVTAQVLSRHGARYPTDSKCKY-SALIEEIQNATTFQGYAFKTKY 98
DB 63 IARDPPGCGVDQVIMYKRGERYPSPSAGKSTEALAKYYSINT-EYKGLAFNDWTY 122
QY 99 SL-----GADDLT-PT-GHQELVNSIKFYQRYESL--TRNIVPFRSSGSRV-ASGK 148
DB 123 YVNECYNAETSGPAGILLDAVNHGNDYKARYGHLWGEVTVVPF-SSGYGRVETAR 191
QY 149 KFTGFGOSTKLQPRAGPGSSPKIDVISEASSKNWLDPGCTCFVDESELADTVEAF 208
DB 182 KFGEGFGYKY-----STNAALNIISESEVMGADSLTP-ICDINDQCTCDNLTYQL 232
QY 209 TATFVPSIRORLENDLGSVTLTDTETVY-VKMGSEDFISTSTVDTKLSPCDLTFHDEW 268
DB 233 PQFVAARLNQSN--PQMNLASDVNVLVMAFSEJNA-----RPFENWNAFTQDEWY 285
QY 269 NYCYLQSLKKYHGAGNPLGPTQGVYANELARLTHSPWHDTSNHTLDSPATFPL 328
DB 286 SFGVVDLNYCYACGPGKQMAVGAIVANASLTLLNQGP-----KEAGP----- 330
QY 329 NSTLYADFSHNGTISILFALGLY--NGTKPLSTTTVENTITQTFSSAWTVFASRLYV 386
DB 331 --LFFNFADHDTNTPILAAAGLVLPEDLPDRVAFSN-----FYSIGNIVPMGGHITI 382

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QY 357 EXMOCCA---EQEPLVRVLVNDVRVPLHGC 413
DB 383 ERLSCQATLSDKGTYYRLVLEAVLPFNDQ 413
RESULT 11
PHYB ASPAK
ID PHYB ASPAK STANDARD: PRT: 479 AA.
AC P34755;
DE 01-FEB-1994 (Rel. 28, Created)
DE 01-FEB-1994 (Rel. 28, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE 3-phytase B precursor (SC 3.1.3.8) (Myo-inositol-hexaphosphate
DE 3-phosphohydrolase B) (pH 2.5 optimum acid phosphatase).
DE PHYB OR APh.
GN Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Peizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
RN [1]_TaxID=105351;
RP SEQUENCE FROM N.A.
RC STRAIN=ALK0243;
RX MEDLINE=94040796; PubMed=8224894;
RA Piddington C.S., Houston C.S., Paloheimo M.T., Cantrell M.A.,
RA Vietinen-Oinonen A., Nevalainen H., Ramosek J.A.;
RT "The cloning and sequencing of the genes encoding phytase (phy) and
RT pH 2.5-optimum acid phosphatase (aph) from Aspergillus niger var.
RT awamori";
RT Gene 133:55-62(1993).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RX MEDLINE=99264417; PubMed=10329192;
RA Kasture D., Wyss M., D'Arcy A., van Loon A.P.;
RT "Crystal structure of Aspergillus niger pH 2.5 acid phosphatase at
RT 2.4-A resolution";
RJ J. Mol. Biol. 288:965-974(1999).
CC -1- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
FROM PHYTATE.
CC -2- CATALYTIC ACTIVITY: Myo-inositol hexakisphosphate + H2O = 1D-
myo-inositol; 1,2,4,5,6-pentakisphosphate + phosphate.
CC -3- SUBUNIT: Homodimer.
CC -4- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
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or send an email to license@isb-sib.ch).
CC
EMBL: J02420; AAA16897.1; .
DR PIR; J02420; AAA16897.1; .
DR PDB; 1QFX; 19-APR-00.
DR InterPro; IPR000560; HisAc phosphatase.
DR Pfam; PF00328; acid phosphatase.
DR PROSITE; PS00616; HIS-ACID-PROSPHAT_1; 1.
DR PROSITE; PS00778; HIS-ACID-PROSPHAT_2; 1.
KW Hydrolase; Glycoprotein; Signal; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 479
FT ACT_SITE 82 82
FT ACT_SITE 337 337
FT DISULFID 71 387
FT DISULFID 128 472
FT DISULFID 216 441
FT DISULFID 225 298
FT DISULFID 413 421
FT CARBOHYD 191 191
FT CARBOHYD 315 315
FT CARBOHYD 458 458
FT HELIX 41 43
FT HELIX 45 47
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)

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SQ SEQUENCE 468 AA; 52690 MW; AE555B8E27718C2C CRC64;
 Query Match 14.0%; Score 327; DB 1; Length 468;
 Best Local Similarity 25.1%; Pred. No. 2.9e-17;
 Matches 112; Conservative 65; Mismatches 179; Indels 92; Gaps 17;
 QY 25 WQVAFPFSLANESVSPVACRVTPFPAVLASHGARYTDSKGGKYKALIEE-LQVNA 83
 DB 62 WG-----IAASEIE-----SCTIDQAHLLMEHGERVPTWVGKLEALYKQLADV 139
 QY 84 TTFQKGVAFKTYNSLGADLTFPQCEVNS-----GKVFQVRESLERNIV 132
 DB 110 EVPTGP-SFQDYCYFVSD---AAWYCEETKGFYSLNTAFDFGTTLRBYDHLNTESE 166
 QY 133 P-----FTRSSGSRVSIASGKFFIEGFQSTKLPFRAQPGOSSPKIDW-SEASSS---NK 193
 DB 167 EGKLSWAGSQERVDVDTAKYFAQGMKSNYTD-----WVEVVALEEEKSQGLAS 216
 QY 186 TLDPGTCT----VFSESELACTV---ENAFATFVPSIRCLRLENDLSGVTLTCTEIVYL 217
 DB 217 LTRISCPNVKSHYKCGFNDIAERADRNLTP-----GFNTADSDIFTI 265
 QY 232 MDKCSFDTISTVDTKLSPPCDLFTHEINVDYLOSLKKYCHGAGPLGPTQGVYA 297
 DB 266 ALVCGPELNVGGE-----SSFCVLSREALITYAYLRDQWYVNGXKPLGKTIGVYA 320
 QY 298 NELLARIETHFVHDRTSSNHLDSPPATPLNSTLPADPSHENGISILFALGJYNGTK- 356
 DB 321 NATRQQLNENT-----EADRDYPT-----LYFSFSDHCDGCGVFTSLGSRVTC 364
 QY 357 PLSTTTVENITOTDGFSSANTVPFASRLYVEMOC--QAEQPLRVLVNLRVTP-HGCP 414
 DB 365 PL-----DQIQFQTSFKSTIIVPMGARLLTERLLCTVEGEEKYVYVTLNDVAFPLSDCS 419
 QY 415 VDALGRCRTDSFVRGLSFARSGGQWAE 441
 DB 420 SGPGFSCPLNDYVSRLEALNEDSDFAE 446
 RESULT 13
 ID -PVAL SCHPO STANDARD; PRT: 453 AA.
 AC P08051;
 CT 01-AUG-1988 (Rel. 08, Created:
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 GN PHO1 CR SP3P4G3.02.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 CX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86140050; PubMed=3005272;
 RA Elliott S., Chang C., Schweingruber M.E., Schaller J., Rickli E.E.,
 CA Carbon J.;
 PT "Isolation and characterization of the structural gene for secreted
 R acid phosphatase from Schizosaccharomyces pombe";
 RJ J. Biol. Chem. 261:2936-2941(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=2184840; PubMed=11859363;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayes J., Baker S., Basham D., Bowmer S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Haldago J., Hodgson G.,
 RA Holroyd S., Howarth T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
 RA James K., Jones L., Jones M., Leather S., McDoraid S., McLean C.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 R Skelton C., Simmonds M., Squares R., Squares S., Stevens K.,
 R Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 R Woodward J., Volkart G., Aert R., Robben J., Grymoprez B.,
 R Well-jers J., Vanstreels E., Rieger M., Schaefer M., Wueller-Auer S.,
 R Gaber C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 R Borym K., Langer I., Beck A., Leinhardt R., Reinhardt R., Pott T.M.,
 R Eger P., Zimmermann W., Wedler H., Wambutt R., Purteille B.,
 R Galliat A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 R Galibert F., Aves S., Xiang Z., Hurt C., Moore K., Hurst S.M.,
 R Lucas M., Rochet M., Gallard J., Tallada V.A., Garzon A., Thode J.,
 R Daga R.R., Cruzado J., Jimenez J., Sanchez M., del Rey F., Benito G.,
 R Dominguez A., Revuelta J.S., Moreno S., Armstrong J., Forsburg S.L.,
 R Cerutti J., Lowe T., McCamble W.R., Paulsen I., Potashkin J.,
 R Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT The genome sequence of Schizosaccharomyces pombe";
 RJ Nature 415:871-880(2002).
 CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
 CC alcohol + phosphate;
 CC -!- SUBCELLULAR LOCATION: Cell wall.
 CC -!- INDUCTION: REPRESSED BY PHOSPHATE AND WEAKLY BY THIAMINE.
 CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 CC
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 CC
 CC EMBL; M11857; AAA35321.1; -;
 CC EMBL; AL137099; CAB8657.1; -;
 CC PIR; A25326; A25326.
 CC HSSP; P14755; 1QFX.
 CC GeneDB Spombe; SPBP4G3.02; -;
 CC InterPro; IPR000560; HisAc phosphatase.
 CC Pfam; PF03328; acid_phosphat; 1
 CC PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1;
 CC PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1;
 CC Hydrolase; Glycoprotein; Cell wall; Signal.
 KW SIGNAL 1 18
 FT CHAIN 19 453
 FT ACT_SITE 69 69
 FT ACT_SITE 330 333
 FT CARBOHYD 95 95
 FT CARBOHYD 151 151
 FT CARBOHYD 183 183
 FT CARBOHYD 193 193
 FT CARBOHYD 243 243
 FT CARBOHYD 319 319
 FT CARBOHYD 410 410
 FT CARBOHYD 429 429
 FT CARBOHYD 443 443
 FT SEQUENCE 453 AA; 50557 MW; 7CF891256EB154D1 CRC64;
 Query Match 12.7%; Score 296.5; DB 1; Length 453;
 Best Local Similarity 24.5%; Pred. No. 5.6e-15;
 Matches 103; Conservative 57; Mismatches 190; Indels 71; Gaps 12;
 QY 18 FSETSHLWQ---YAPFSLANESVISPEV---PAGCRVTFACVLSRHGARYPTDSKGGKY 72
 DB 30 PDFKRELTSRSPYHKPYF-----YGPSIDPFTCKIKQVHTLQRHGSNPTGNAAFD 82
 QY 73 SALIEEIQQ-----NATTFDGKAFKLYTN---YSLGADLTFPQCEVNSGIKF 120
 DB 83 AVGIANFQORLLNGSVPIDYVSGNPLSFVPTWTPVIEAANADALSSSGRVELFDMGRQF 142
 QY 121 YQVESLTRNVIPFIRSSGSSRVSIASGKFF-----IEGFQSTKLPFRAQFGQSSPK 172
 DB 143 YERYHELFENASTYNIYTAQQRVVDSSALWYGYGMFGEDVHNTYVILVSENATAGSSN-- 200

QY 173 IDWVISESSSNTLDPGTCVFESELDATVEANFTATFVFSRQRLNLSGLTUT 232
 DB 201 -----SSYN-----ACASADDDFTTALAEARNVWPPRQRENPFYSYNLTND 247
 QY 233 EYVYVDMCSFPTSTVTKLSPFCDLFTHDEKINVDYLOSKKYVGHGAGNLPQTQ 292
 DB 248 DILNLYGICSEIALQC-----YSEFCKLNSVDFNFEYEGDLFSYGMGNSYKWSIF 332
 QY 293 GVGYNELARLTHSPVHDOTSSNHTLSSPATFPLKSLTVADESHDNGIISLIFALGLY 352
 DB 303 GAYANSLANSR-----SVENNT-----QQFFATHOAKLIPETALGFF 344
 QY 353 NGTKPLSTTVENITQTCGFSSAVTPFASRYVEMMCQAEQFPVRLVNVDAWVPLHG 412
 DB 345 TDNTPENPLFTSYOVHSHMSKASRFVPFAGNLITELPQCE-DSKYVVRHLVNEEVFLSD 463
 QY 413 C 413
 DB 404 C 404

RESULT 14
 PP22_SCHPO
 ID PP22_SCHPO STANDARD; PRT: 463 AA.
 AC Q01682; Q90U70;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Thiamine-repressible acid phosphatase precursor (BC 3.1.3.2).
 GN PH04 CR SP8C428.33C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID:4896;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 19-30.
 RX MEDLINE=91064763; PubMed=2249257;
 RA Yang J., Schweingruber M.E.;
 RT "The structural gene coding for thiamine-repressible acid phosphatase
 RT in Schizosaccharomycetes pombe.";
 RL Curr. Genet. 18:269-272(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=2184840; PubMed=11859360;
 RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Spouris J., Peat N., Hayles J., Baker S., Chillingworth T., Churcher C.M.,
 RA Brooks K., Brown D., Brown S., Davis P., Feltwell T., Fraser A.,
 RA Collins M., Connor R., Cronin A., Harris D., Hidalgo J., Hodgson G.,
 RA Gentles S., Geble A., Hamlin N., Hartis D., Hiderg J., Jorgensen K.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones J., Jones M., Leather S., McDonald S., McLean C.,
 RA Mooney P., Moule S., Mungall K., Murphy S., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Shelton C., Simmonds R., Squares R., Squares S., Stevens K.,
 RA Stelton C., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward C., Wolcott G., Aert R., Robben J., Grynprenz B.,
 RA Weitzens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann M., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreazo S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gallard C., Tallada V.A., Garzon A., Rhode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta G.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen O., Petastkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomycetes pombe.";
 RL Nature 415:871-880(2002).
 RN [3]

SEQUENCE OF 1-71 FROM N.A.
 RC STRAIN=968 b30;
 RX MEDLINE=2022868; PubMed=1075989;
 RA Ding D.-Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,
 RA Hiraoka Y.;
 RT "Large-scale screening of intracellular protein localization in living
 RT fission yeast cells by the use of a GFP-fusion genomic DNA library.";
 RL Genes Cells 5:169-193(2000).
 CC - FUNCTION: MAY DEPHOSPHORYLATE THIAMINE PHOSPHATES.
 CC - CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
 CC alcohol + phosphate.
 CC - SUBCELLULAR LOCATION: Cell wall.
 CC - INDUCTION: Repressed by thiamine.
 CC - SIMILARITY: BELONGS TO THE H-STEADINE ACID PHOSPHATASE FAMILY.
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 CC
 CC EMBL: X56939; CAA40258.1; ..
 CC EMBL: AL034382; CAA22278.1; ..
 CC EMBL: AB027777; BAA8708.1; ..
 CC PIR: S14119; S14119.
 CC HSP: P34755; 1QFX.
 CC GeneDB SPORBE; SP8C428.C3C; ..
 CC InterPro: IPR000560; HisAc_phosphatase.
 CC Pfam: PF00328; acid_phosphat_1; 1.
 CC PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.
 CC PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.
 KW Hydrolase; Glycoprotein; Cell wall; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 463
 FT ACT_SITE 69
 FT ACT_SITE 340
 FT CARBOHYD 98
 FT CARBOHYD 104
 FT CARBOHYD 186
 FT CARBOHYD 221
 FT CARBOHYD 251
 FT CARBOHYD 328
 FT CARBOHYD 433
 FT CARBOHYD 439
 FT CARBOHYD 458
 SO SEQUENCE 463 AA; 52118 MW; P48EAF8B85234A CRC64;
 Query Match 12.2%; Score 284; DB 1; Length 463;
 Best Local Similarity 24.9%; Pred. No. 5,1e-14;
 Matches 102; Conservative 56; Mismatches 181; Indels 60; Gaps 13;
 QY 28 YAPFSLANESVISPEVAGGRVTFQVLSHGARYP-----TDSKGYKYSALIE----- 77
 DB 43 HSPYNGFTTS-----PPESCAKQVHLLQRHGSRNPTGDDTATDVSSAQVDFQKLL 97
 QY 78 --EIQONATTPDGKVAFLKTNYSJ---GADLTFFGCELVNSGKIFYORYESLTNIV 132
 DB 98 KGSIPVNFSPENPYFVHHWTPVKAENAOQLSSGRZELDFGRQVFEYEFDTDV 157
 QY 133 PFIIRSGSRVSIASGKKTIEGFTKLMDPRAQPGSQSPKIDVVI---SEASSNNITLDP 189
 DB 158 YDINTAAQERVVDASAEWSYGFQGDMDQN-----KCNFVLFEEDSAGANSAMY 207
 QY 190 GTCVFESESEL-ADTVEANFTA---TFVPSIRQRLNLSGLTUTVYLMDCMSFD 244
 DB 208 YSCPYFENNIDENTTEAAHTSWARNFLKPIANKLNKYFDSGYNLTVDVRSYVIVYE 267
 QY 245 TISTSTVTIKLSPPCOLFTTHDEWINVDYLOSLLKKYVGHGAGNPLGPTQGVYANELLARL 304
 DB 268 IALRNSD-----FCSLTFPSEFLNFEYDSDLDVAYWGPASEWASTLGGYVNNLANL 322

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QY 305 TSPVHDDTSSNHTLSSPATFENSTLVADFHDNGHIIISLFAJGYNVNGTFFPLSTTIVE 364
Cc 323 R-----KGVNASORK-----VFLAFTHDSQIIPVEAALGFPPDITPERPLPTD 366
QY 365 NITCTDGFSSAKTVFASRLYVEMMOCAOEPLVAVLNDRVVPLHGC 413
Cc 367 KNIFTYSLKTSVFFAGNITLFLC-SNKYVYVRLVNOQVYPLTDC 414

RESULT 15
AGP_ECOLI
ID_AGP_ECOLI: STANDARD; PRT; 413 AA.
AC P1936;
DT 01-FEB-1992 (Rel. 17, Created);
DT 01-FEB-1991 (Rel. 17, Last sequence update);
DT 16-OCT-2001 (Rel. 40, Last annotation update);
DE Glucose-1-phosphatase precursor (EC 3.1.3.10) (G.Pase).
GN AGP CR B1032.
OS Escherichia coli.
CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
CC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1];
RS SEQUENCE FROM N.A., AND SEQUENCE OF 23-31.
RC STRAIN=K12;
MEDLINE=90130118; Pubmed=21513660;
RA Pradel E., Varcok C., Boquet P.L.;
R "Nucleotide sequence and transcriptional analysis of the Escherichia coli agp gene encoding periplasmic acid glucose-1-phosphatase.";
PL J. Bacteriol. 172:802-807(1990).
RN [2];
RS SEQUENCE FROM N.A.
RC STRAIN=K12;
MEDLINE=9742661; Pubmed=9278503;
RA Battner F.R., Plunkett G. Jr., Bloch C.A., Perna N.R., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
R "The complete genome sequence of Escherichia coli K-12.";
PL Science 277:1453-1474(1997).
RN [3];
RS SEQUENCE FROM N.A.
RC STRAIN=K12;
MEDLINE=97061202; Pubmed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara K., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
R "A 7.8-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
PL DNA Res. 3:137-155(1996).
RN [4];
RS SEQUENCE OF 23-34.
RC STRAIN=K12 / EMG2;
MEDLINE=97443975; Pubmed=9298646;
RA Link A.J., Robison K., Church G.M.;
R "Comparing the predicted and observed properties of proteins encoded in the genome of Escherichia coli K-12.";
RL Electrophoresis 18:1259-1313(1997).
CC -!- FUNCTION: ABSOLUTELY REQUIRED FOR THE GROWTH OF E. COLI IN A HIGH-PHOSPHATE MEDIUM CONTAINING G-1-P AS THE SOLE CARBON SOURCE.
CC -!- CATALYTIC ACTIVITY: D-glucose 1-phosphate + H(2)O = D-glucose + phosphate.
CC -!- ENZYME REGULATION: INDEPENDENT FROM INORGANIC PHOSPHATE AVAILABILITY, AND APPARENTLY SUBMITTED TO CATABOLITE REPRESSION.
CC IT IS POSITIVELY CONTROLLED BY CAMP AND THE CAMP RECEPTOR PROTEIN.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Periplasmic.
CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
```

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Cc -----
Cc EMBL; M33807; AAA23426.1;
Cc EMBL; AEC00202; AAC74087.1;
Cc EMBL; C90737; BAA35769.1;
Cc EMBL; D90738; BAA35779.1;
Cc EMBL; J90887; J90887.
Cc HSP; F07102; LDKV.
Cc EcoGene; EG-0033; agp.
Cc InterPro; IPR00560; H:Sac phosphatase.
Cc Pfam; PF00328; acid phosphatase; 1.
Cc PROSITE; PS02616; H2S ACID PHOSPHAT 1; 1.
Cc PROSITE; PS02778; H2S ACID PHOSPHAT 2; 1.
Cc Hydrolase; Periplasmic; Signal; Complete proteome.
Cc SIGNAL 1 22
Cc CHAIN 23 413 GLUCOSE-1-PHOSPHATASE.
Cc ACT SITE 40 40 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
Cc ACT SITE 311 311 PROTON DONOR (BY SIMILARITY).
Cc SEQUENCE 413 AA; 45683 MW; ADADAD3639D0D6AB CRC64;

Query March 5, 1998; Score 119.5; DR 1; Length 413;
Best Local Similarity 22.04; Freq. No. 3.2; Indels 155; Gaps 22;
Matches 101; Conservative 40; Mismatches 163;

QY 44 VFAGRVTFAGVLSRHGAFVPTSGKSKYKSALEIEIQNATTFGKYAFKTYNYSIGAD 103
Cc 25 VFEQVQLCQVLMKSRHNPAPLANNG-----SVLEQSTPN-----KWENQVPGG 69
QY 104 DLTFFG-----EQELVNSG-----IKFYQRYESLTHNIVPFIRSSGSSR 142
Cc 70 QLTTKGVLEVYMGHYMREMLAEQGVKSGCEPPYTVYAYANSL-----QR 116
QY 143 VIASCKKTEGFQSTKLKCPAPQSGSSPKIDVWSEASSNNITLDRGCTVFEDELAD 202
Cc 117 TVATAQFFITG-----AFPGCDIP-----VHHQKMGTMPTFNFVITCD 156
QY 203 TVEANFTATFVPSIRQRIENDLSGVTLTDT-----VTYL-----MDMCSF-----DT 245
Cc 157 -----SNAFSEQVAAVEKELSKLQITDSVQLLEKIVNPKDSKPACKEKCCSVDGKNT 210
QY 246 IS-----TSTVDTKLSPFCDFTHDE--W-----INYLQSLKKYVG 281
Cc 211 FSARYQCEPPGVSGELPKVGNLSVDFTQYVEGFFYDQVAKGEIKSDQQWYVSKLXGYQ 270
QY 282 HGAGNPLGPTQGVYANELIARLTHSPVHDTSSNHTLSSPATFPLNSTLYADPFSHDNG 341
Cc 271 DSLFT--SPEVARNVAKPLVSVIDKALVTRTSA-----PKITVL-----VGHDSN 314
QY 342 IISILFALGLYNGTKPLSTTTVENITQDGF--FSSANTVPFASR--LYVENMQQAS--- 394
Cc 355 IASLITALDF---KPYQLHDQNETRTPIGKIVFORWHDKSKANRLMKIEVYVQSAEQLR 370
QY 395 -----QEPLVRVLVNDRVVPLHGCPCVDALGCRTRDSF 426
Cc 371 NADALTLOAPQARV-----TLELSGCPIDADGFCFMDKF 404

Search completed: November 12, 2003, 14:31:56
Job time : 19 secs
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Db 264 CSPTTISTSTVCTKLSDFCCLFTHDEWINDYLOSILKKYVGHGAGNPLGPTQGVYANEL 323
 QY 301 IARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLST 360
 Db 324 IARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLST 383
 QY 361 TTVENITQTDFSSAWTVFPASRLYVEMMQCAEQEPLVRVLVNDRWVPLRGCPVDALGR 420
 Db 384 TTVENITQTDFSSAWTVFPASRLYVEMMQCAEQEPLVRVLVNDRWVPLRGCPVDALGR 443
 QY 421 CTRDSFVRGLSFARSGGDWAE 444
 Db 444 CTRDSFVRGLSFARSGGDWAE 467

RESULT 2
 JN0482
 3-phosphate (EC 3.1.3.8) A - Aspergillus ficuum
 N:Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phya protein
 C:Species: Aspergillus ficuum
 C:Date: 30-Sep-1993 #sequence_revision 10-Oct-1995 #ext_change 07-May-1999
 C:Accession: JN0482; PNC023
 R:Ullah, A.H.S.; Dischinger Jr., H.C.
 Biochem. Biophys. Res. Commun. 192, 747-753, 1993
 A:Title: Aspergillus ficuum phytase: Complete primary structure elucidation by chemical
 A:Reference number: JN0482; MUID:93249451; PMID:8387289
 A:Accession: JN0482
 A:Molecule type: protein
 A:Residues: 1-44; <JUL>
 A:Note: authors state that the 9 Asn followed by Thr or Ser after an intervening residue
 R:Ullah, A.H.S.; Cummins, B.J.; Dischinger Jr., H.C.
 Biochem. Biophys. Res. Commun. 178, 45-53, 1991
 A:Title: Cyclohexanediol modification of arginine at the active site of Aspergillus fic
 A:Reference number: PNC023; MUID:93298982; PMID:1648914
 A:Accession: PNC023
 A:Molecule type: protein
 A:Residues: 48-70 <UL2>
 C:Comment: This enzyme catalyzes the hydrolysis of inorganic orthophosphate from phytate
 C:Superfamily: yeast acid phosphatase
 C:Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phosph
 F:436,82,97,194,207,316,329,353,365/Binding site: carboxylate (Asn) (covalent) #status
 F:58/338/Active site: Arg, His #status predicted
 F:59/Active site: His (phosphohistidine intermediate) #status predicted

Query Match 99.2%; Score 2315; DB 1; Length 447;
 Best Local Similarity 100.0%; Pred. No. 8.3e-162;
 Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASRNOSSCDTVDOGYQCFSETSHLWQYAFPPFSLANESVLSPEVPAGCRVTRACVLSRHG 60
 Db 1 ASRNOSSCDTVDOGYQCFSETSHLWQYAFPPFSLANESVLSPEVPAGCRVTRACVLSRHG 60
 QY 61 ARYPTDSKGGKYSALIEEIQONATTFDGYAFPLKTYNSLGADCLTFPGEQELVNSGIXF 120
 Db 61 ARYPTDSKGGKYSALIEEIQONATTFDGYAFPLKTYNSLGADCLTFPGEQELVNSGIXF 120
 QY 121 YQRYESLTRNIVPFISSGSRVLSGKKFIEGFQSTKLPKPAQPCQSSPKIDVYISEA 180
 Db 121 YQRYESLTRNIVPFISSGSRVLSGKKFIEGFQSTKLPKPAQPCQSSPKIDVYISEA 180
 QY 181 SSSNNTLDPGCTCTVFEDSELADTVEANFTATFVPSIRQRLENDSGLVTLTDEVTYLMOM 240
 Db 181 SSSNNTLDPGCTCTVFEDSELADTVEANFTATFVPSIRQRLENDSGLVTLTDEVTYLMOM 240
 QY 241 CSFDTISTSTVDTKLSPPCDLFTHEWINDYLOSILKKYVGHGAGNPLGPTQGVYANEL 300
 Db 241 CSFDTISTSTVDTKLSPPCDLFTHEWINDYLOSILKKYVGHGAGNPLGPTQGVYANEL 300
 QY 301 IARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLST 360
 Db 301 IARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLST 360
 QY 361 TTVENITQTDFSSAWTVFPASRLYVEMMQCAEQEPLVRVLVNDRWVPLRGCPVDALGR 420

Db 362 TTVENITQTDFSSAWTVFPASRLYVEMMQCAEQEPLVRVLVNDRWVPLRGCPVDALGR 420
 QY 421 CTRDSFVRGLSFARSGGDWAE 441
 Db 421 CTRDSFVRGLSFARSGGDWAE 441

RESULT 3
 JN0859
 3-phytase (EC 3.1.3.8) A precursor - Aspergillus awamori
 N:Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phya protein
 C:Species: Aspergillus awamori
 C:Date: 14-Jul-1994 #sequence_revision 19-Oct-1995 #ext_change 11-Jun-1999
 C:Accession: JN0859
 R:Poddington, C.S.; Houston, C.S.; Palohermo, M.; Castrell, M.; Miettinen-Oinonen, A.
 Gene 133, 55-62, 1993
 A:Title: The cloning and sequencing of the genes encoding phytase (phy) and pH 2.5-op
 A:Reference number: JN0859; MUID:94040796; PMID:8224894
 A:Accession: JN0859
 A:Molecule type: DNA
 A:Residues: 1-467 <PID>
 A:Cross-references: GB:D32421; NID:G:66519; PID:AAA16998.1; PID:G:66519
 A:Experimental source: strain ALK0243
 A:Note: part of the sequence, including the amino end of the mature protein, was conf
 C:Comment: This enzyme catalyzes the conversion of phytate to inositol and inorganic
 C:Genetics:
 A:Gene: phya
 A:Introns: 15/2
 C:Superfamily: yeast acid phosphatase
 C:Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; ph
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-467/Product: 3-phytase A #status experimental <MAT>
 F:27,59,105,120,207,230,339,352,376,388/Binding site: carboxylate (Asn) (covalent) #
 F:81/361/Active site: Arg, His #status predicted
 F:82/Active site: His (phosphohistidine intermediate) #status predicted

Query Match 98.1%; Score 2290; DB 1; Length 467;
 Best Local Similarity 97.3%; Pred. No. 6.1e-160;
 Matches 432; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASRNOSSCDTVDOGYQCFSETSHLWQYAFPPFSLANESVLSPEVPAGCRVTRACVLSRHG 60
 Db 24 ASRNOSSCDTVDOGYQCFSETSHLWQYAFPPFSLANESVLSPEVPAGCRVTRACVLSRHG 82
 QY 61 ARYPTDSKGGKYSALIEEIQONATTFDGYAFPLKTYNSLGADCLTFPGEQELVNSGIXF 120
 Db 84 ARYPTDSKGGKYSALIEEIQONATTFDGYAFPLKTYNSLGADCLTFPGEQELVNSGIXF 143
 QY 121 YQRYESLTRNIVPFISSGSRVLSGKKFIEGFQSTKLPKPAQPCQSSPKIDVYISEA 180
 Db 144 YQRYESLTRNIVPFISSGSRVLSGKKFIEGFQSTKLPKPAQPCQSSPKIDVYISEA 202
 QY 181 SSSNNTLDPGCTCTVFEDSELADTVEANFTATFVPSIRQRLENDSGLVTLTDEVTYLMOM 240
 Db 204 SSSNNTLDPGCTCTVFEDSELADTVEANFTATFVPSIRQRLENDSGLVTLTDEVTYLMOM 263
 QY 241 CSFDTISTSTVDTKLSPPCDLFTHEWINDYLOSILKKYVGHGAGNPLGPTQGVYANEL 300
 Db 264 CSFDTISTSTVDTKLSPPCDLFTHEWINDYLOSILKKYVGHGAGNPLGPTQGVYANEL 323
 QY 301 IARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLST 360
 Db 324 IARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLST 383
 QY 361 TTVENITQTDFSSAWTVFPASRLYVEMMQCAEQEPLVRVLVNDRWVPLRGCPVDALGR 420
 Db 384 TTVENITQTDFSSAWTVFPASRLYVEMMQCAEQEPLVRVLVNDRWVPLRGCPVDALGR 443
 QY 421 CTRDSFVRGLSFARSGGDWAE 444
 Db 444 CTRDSFVRGLSFARSGGDWAE 467

submitted to the Protein Sequence Database, August 1994

A:Reference number: S45927
A:Accession: S45960
A:Molecule type: DNA
A:Residues: 1-467 <PE2>
A:Cross-references: EMBL:Z35961; NID:G516362; PIDN:CAA85045.1; PID:G516363; GSPDB:GN5000
R:Balwa, W.; Meyhack, B.; Rudolph, H.; Schweingruber, A.M.; Hinnen, A.
Nucleic Acids Res. 22, 7721-7739, 1994
A:Title: Structural analysis of the two tandemly repeated acid phosphatase genes in yeast
A:Reference number: SCS794; MUID:85037940; PMID:6053051
A:Accession: SCS794
A:Molecule type: DNA
A:Residues: 1-218, 'EMBL', 222-467 <BAJ1>
A:Cross-references: EMBL:X01080; NID:G4148; PIDN:CAA25557.1; PID:G759281
A:Note: the authors translated the codon AAT for residue 134 as Asp and TAC for residue
R:Rait-Kamradt, A.G.; Turner, K.J.; Kramer, R.A.; Elliott, G.D.; Scsian, S.J.; Thill, G.
Mol. Cell. Biol. 6, 1855-1865, 1986
A:Title: Reciprocal regulation of the tandemly duplicated PHO5/PHO3 gene cluster within
A:Reference number: A93074; MUID:87064474; PMID:3537710
A:Accession: A25241
A:Molecule type: DNA
A:Residues: 1-44 <TA1>
C:Genetics:
A:Gene: SGD:PHO3; MFS:YBR092C
A:Cross-references: SGD:SC000236; MIPS:YBR092C
A:Map position: 2R
C:Superfamily: Yeast acid phosphatase
C:Keywords: glycoprotein; phosphatidine; phosphoprotein; phosphoric monoester hydrolase
F:1-17/Domain: signal sequence; #status predicted <SIG>
F:18-467/Product: acid phosphatase, constitutive #status predicted <ANT>
F:75/Active site: His (phosphatidine intermediate) #status predicted
F:97,103,162,192,250,315,356,390,439,445,456,461/Binding site: carbohydrate (Asn) (coval
F:337/Active site: His #status predicted

Query Match 16 58; Score 385; DB 1; Length 467;
Best Local Similarity 26.18; Pred. No. 1.9e-50;
Matches 113; Conservative 63; Mismatches 195; Indels 62; Gaps 11;
QY 26 GQYAPFSLANESV:SPVPAGCRVTFQVLSRHGARYPTDSKGYKYSALIEIQNATT 65
DB 42 GGAGPYSPFCGYC:SRDLPGCEMKQLQMLRHGERYPYSGATIMKTWYKLSNYTRQ 101
QY 86 FDGYAFILK-TYNSLGADD-----LTFP-GEQLVNSGKIFQPIRESLJR 129
DB 102 FNGSLSPFUNDYEFIRDDOLEMETTANSNDVNPYTGEMAKAHAREFLAKYKLM 161
QY 130 NIVFP-IRSSGSRVIAAGKAFIEGFCSTKLKOPRAQPGQSSPKIDVY-SEASSNLTLD 188
DB 162 NQTSFP-FAASSERVHOTAQYFDG-----LGD-----QFNISLQTVSEAMGAGANTLS 210
QY 189 PGTCTVPEDSELADTVENFTATVPISIRGLENDLSGVTLTTEVTYIMDKSCFDTIST 248
DB 211 AGNACPGWCEANDDILCKYDTYLDJIAKRLKENKGNLTSCANTLFAWCAVEANAR 270
QY 249 STVDTKLSPFDLTHDEW:NVQYLSKLYYGGAGNP:SPQGGYGANELIARITHSP 308
DB 271 GYSDV-----CDITFEDELKRYSGQDLVSPYQDGPYDMIRSVGAKLFNATLKLKQSE 325
QY 339 VHDTSNHTLDSSPATFPLNSTLYADFSHNGTISILFALGLYNGTKPLSTTTTIV 368
DB 326 TQC-----LKWLSFTHTDILNLTITTAG:IDCKNNTABYVPPFMGN 367
QY 369 TDGFSAMTVPFASRLVYVEMMQCAEQEPLVRVLVNDRVVPLHSCPYDALGRCITRDF-- 426
DB 368 T--PHKSYVVGARVYTEKFC--SNDTYRVYVINDAVVPIETCTGPGFSCE:INDFD 423
QY 427 -----VRGLSFAR 434
DB 424 YAEKRVAGTDFLK 436

RESULT 6
SS2495

acid phosphatase homolog YD024c - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein D2815
C:Species: Saccharomyces cerevisiae
C:Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 19-Apr-2002
C:Accession: S52495; S67556
R:Andre, B.; Visser, S.; Urestarazu, L.
submitted to the EMBL Data Library, February 1995
A:Description: The sequence of a 42 kb segment located on the left arm of chromosome
A:Reference number: S52492
A:Accession: S52495
A:Molecule type: DNA
A:Residues: 1-468 <AND>
A:Cross-references: EMBL:Z48432; NID:G683669; PIDN:CAA89335.1; PID:G683673
A:Experimental source: strain S288C
R:Urestarazu, L.A.; Andre, B.; Visser, S.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67556
A:Accession: S67556
A:Molecule type: DNA
A:Residues: 1-468 <URR>
A:Cross-references: EMBL:Z74072; NID:G1430996; PIDN:CAA98593.1; PID:G1430997; MIPS:YD
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:DIA3
A:Cross-references: SGD:SC002182
A:Map position: 4L
C:Superfamily: yeast acid phosphatase

Query Match 15 88; Score 368; DB 2; Length 468;
Best Local Similarity 25.08; Pred. No. 3.4e-19;
Matches 109; Conservative 74; Mismatches 181; Indels 72; Gaps 13;
QY 26 GQYAPFSLANESV:SPVPAGCRVTFQVLSRHGARYPTDSKGYKYSALIEIQNATT 85
DB 43 GGSAPYSPFANYG:IPDIPEGCRITQVQMCRHGERYPTREAKDIFEWYKISNYTCK 102
QY 86 FDGYAFILK-TYNSL-----GADDLTFP-GEQLVNSGKIFQPIRESLJR 129
DB 103 YEGSLSPFNGYEFF-PDESLLMETTLQNS:DLVNPYTGEMAKAHAREFLAKYKLM 162
QY 130 NIVFP-IRSSGSRVIAAGKAFIEGFCSTKLKOPRAQPGQSSPKIDVY-SEASSN 184
DB 163 NCNFPITNSKRIYDTACYPALALGDGPNIS-----LQTLSENSSSGA 207
QY 185 NTLOPGTCTVFDESELAQTVENFTATVPISIRGLENDLSGVTLTTEVTYIMDKSCF 244
DB 208 NTLAAKSCPMWNSKANDILKYSRDY:LENISDRUNDENKGLNSRDAALFQWCAFE 267
QY 245 TISTSTVDTK-LGSPFDLTHDEW:NVQYLSKLYYGGAGNP:SPQGGYGANELIAR 303
DB 268 -----LNAGYSNICDIFSAELIHYSVETDLTSPYQNGPYKLIKSGANLFNATV-K 320
QY 304 LTHSPVHDDTSKNTLDDSPATFPLNSTLYADFSHNGTISILFALGLYNGTKPLSTTTIV 363
DB 321 LIROSA-----LQKWLSTHTDILNLTITTAG:LDTRNCTTNEV 363
QY 364 ENITQTDGFSAMTVPFASRLVYVEMMQCAEQEPLVRVLVNDRVVPLHSCPYDALGRCITR 423
DB 364 P--PHKSYVVGARVYTEKFC--SNDTYRVYVINDAVVPIESCSGPGFSCE 413
QY 424 DSF-----VRGLSF 432
DB 420 GTFVEYAKDRILRGVSF 435

RESULT 7
SS3476

acid phosphatase (EC 3.1.3.2) precursor - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YAR071w
C:Species: Saccharomyces cerevisiae
C:Date: 05-May-1995 #sequence_revision 01-Sep-1995 #text_change 20-Apr-2000
C:Accession: S53476; JCI018
R:Bussey, H.; Keng, T.; Storms, R.K.; Vo, D.; Zhong, W.; Fortin, N.; Barton, A.B.; K

submitted to the EMBL Data Library, February 1994
A:Description: Sequencing of chromosome I of *Saccharomyces cerevisiae*: analysis of the S
A:Reference number: S53458
A:Accession: S53476
A:Molecule type: DNA
A:Residues: 1-467 <BUS>
A:Cross-references: EMBL:J28920; NID:91616966; PIDN:AAC9503.1; PID:9456155; MIPS:YAR071
A:Chen, J.Y.; Gong, Y.; Ao, S.Z.
Acta Biochim. Biophys. Sin. 21, 437-444, 1989
A:Title: The primary structure of acid phosphatase gene PHO1 in *S. cerevisiae* and compa
A:Reference number: JCI018
A:Accession: JCI018
A:Molecule type: DNA
A:Residues: 1-16, 'L', 18-149, 'H', 151-422, 'G', 424-467 <CHE>
A:Note: this paper is in Chinese, with an English abstract
C:Genetics:
A:Gene: SGD:PHO1
A:Cross-references: SGD:S0000094; MIPS:YAR071W
A:Map position: 1R
C:Superfamily: yeast acid phosphatase
C:Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester; hydroly
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-467/Product: acid phosphatase #status predicted <Mat>
F:74/Active site: Arg #status predicted
F:75/Active site: His (phosphohistidine intermediate) #status predicted
F:97,162,192,250,315,356,439,445,461/Binding site: carbohydrate (Asn) (covalent) #status
Query Match 15.1%; Score 352; DB 2; Length 467;
Best Local Similarity 24.4%; Pred. No. 5.1e-18;
Matches 107; Conservative 70; Mismatches 189; Indels 72; Gaps 14;
CY 26 GYAPFESLANESVSPVAGCEVTFPAQVSRHGARYPTDSKGYKYSALIEIQNATT 85
DB 42 GSGPYYSFGDYGISRDLPESCCEMKQVQVGRHGERYPTVSKAKSMTTWYKLSNYTGQ 101
CY 86 FCGYAFK-----YNYVS-----GADLTFF-GEQELVNSGIRFYQRYESLTR 129
DB 102 FSGALSFLNDYEFFRDTKNLEMETLANSVNVNPNYTGEMNAKRHARDFLAQYGYWE 161
CY 130 NIVVP--RSGSSRVASGKFFEGFQSTKLDPRAPQGSQSPKIDV---VSEASSN- 184
DB 162 NQTSFAVFTSNRCHDTAQYFDGL-----GSKFNISLQT--SEASAGA 206
CY 185 NTLDP-GTCTVEDSLATVEANFTATFVPSIRQRLNDLSGVLTDTTEVYLMDCSF 243
DB 207 NTLAHSHPAMDQ--QVNDQILKKYDTKYLGLAKRLNKENKGLNLTSSDANTFFAWCAY 265
CY 244 DTISTSTVDTKLSFFCDLFTHEWINDYQLSKYKYGAGNPLGPTQGVYANELIAR 303
DB 266 EINARG-----YSDICNITKDELVRFSYQDLETTYQTGPGYDVVRSGANLFNASVKL 320
CY 304 JTHSPVHDOTSSNHTLDSPPATFPLNSTLYAFSPHNGIISILFALGLYNGTKPLSTTTV 363
DB 321 LKSEVQD-----QKWLSTHDTDLNLT--TIGIIDCKNNLTAHV 362
CY 364 ENITQDGSSEANTVPASRLYVEMMQCAEQEPPLVRVLVNDVRVPLHGCVDALGRCTR 423
DB 363 PMENT--FHRSWYVQGARVYTEKFC--SNDTYVRVINDAVVPIETCTSTGPGFSCEI 419
CY 424 DSF-----VRGLSPAR 434
DB 419 NDFYDVAEKVAGCTDFLK 436
RESULT 8
S48996
N:Alternate names: PHO12 - yeast (*Saccharomyces cerevisiae*);
C:Species: *Saccharomyces cerevisiae*
C:Date: 02-Dec-1994 #sequence_revision: 02-Dec-1994 #text_change 22-Jun-1999
A:Accession: S48996; S59659
R:Macri, C.
submitted to the EMBL Data Library, February 1994

A:Description: The sequence of *S. cerevisiae* cosmid 9.77.
A:Reference number: S46671
A:Accession: S48996
A:Molecule type: DNA
A:Residues: 1-467 <MAC>
A:Cross-references: EMBL:U00029; NID:9551322; PIDN:AAB69729.1; PID:9458917; MIPS:YHR21
R:Xi, L.
submitted to the EMBL Data Library, January 1995
A:Reference number: S59658
A:Accession: S59659
A:Molecule type: DNA
A:Residues: 1-16, 'L', 18-81, 'AB', 84-149, 'H', 151-467 <XUL>
A:Cross-references: EMBL:J19789; NID:9847754; PIDN:AAA73479.1; PID:9847755
C:Genetics:
A:Gene: SGD:PHC12
A:Cross-references: SGD:S0001258; MIPS:YHR215W
A:Map position: 8R
C:Superfamily: yeast acid phosphatase
C:Keywords: phosphoric monoester hydrolase
Query Match 15.1%; Score 352; DB 2; Length 467;
Best Local Similarity 24.4%; Pred. No. 5.1e-18;
Matches 107; Conservative 70; Mismatches 189; Indels 72; Gaps 14;
CY 26 GYAPFESLANESVSPVAGCEVTFPAQVSRHGARYPTDSKGYKYSALIEIQNATT 85
DB 42 GSGPYYSFGDYGISRDLPESCCEMKQVQVGRHGERYPTVSKAKSMTTWYKLSNYTGQ 101
CY 86 FCGYAFK-----YNYVS-----GADLTFF-GEQELVNSGIRFYQRYESLTR 129
DB 102 FSGALSFLNDYEFFRDTKNLEMETLANSVNVNPNYTGEMNAKRHARDFLAQYGYWE 161
CY 130 NIVVP--RSGSSRVASGKFFEGFQSTKLDPRAPQGSQSPKIDV---VSEASSN- 184
DB 162 NQTSFAVFTSNRCHDTAQYFDGL-----GSKFNISLQT--SEASAGA 206
CY 185 NTLDP-GTCTVEDSLATVEANFTATFVPSIRQRLNDLSGVLTDTTEVYLMDCSF 243
DB 207 NTLAHSHPAMDQ--QVNDQILKKYDTKYLGLAKRLNKENKGLNLTSSDANTFFAWCAY 265
CY 244 DTISTSTVDTKLSFFCDLFTHEWINDYQLSKYKYGAGNPLGPTQGVYANELIAR 303
DB 266 EINARG-----YSDICNITKDELVRFSYQDLETTYQTGPGYDVVRSGANLFNASVKL 320
CY 304 JTHSPVHDOTSSNHTLDSPPATFPLNSTLYAFSPHNGIISILFALGLYNGTKPLSTTTV 363
DB 321 LKSEVQD-----QKWLSTHDTDLNLT--TIGIIDCKNNLTAHV 362
CY 364 ENITQDGSSEANTVPASRLYVEMMQCAEQEPPLVRVLVNDVRVPLHGCVDALGRCTR 423
DB 363 PMENT--FHRSWYVQGARVYTEKFC--SNDTYVRVINDAVVPIETCTSTGPGFSCEI 419
CY 424 DSF-----VRGLSPAR 434
DB 419 NDFYDVAEKVAGCTDFLK 436
RESULT 9
JN0715
3-phytase (EC 3.1.3.8) B precursor - *Aspergillus ficum*
N:Alternate names: pH 2.5-optimum acid phosphatase
C:Species: *Aspergillus ficum*
C:Date: 14-Jul-1994 #sequence_revision 19-Oct-1995 #text_change 07-May-1999
A:Accession: JN0715; P0594; P0460
R:Enrich, K.C.; Montalbano, B.G.; Mullaney, E.J.; Dischinger G., H.C.; Ullah, A.H.J.
Biochem. Biophys. Res. Commun. 195, 53-57, 1993
A:Title: Identification and cloning of a second phytase gene (phyB) from *Aspergillus n*
A:Reference number: JN0715; MUID:93371452; PMID:7916610
A:Accession: JN0715
A:Molecule type: DNA
A:Residues: 1-479 <ERR>
A:Cross-references: GB:L20567
A:Accession: P0594


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Db 62 WG-----IAASEIE-----SCTDQAHLLVRHGERYFSTNVGQLEALYKQLDADV 109
QY 84 TTFDGKFAFKTNYSIGADELTPFGQELVNS-----GKFKYQRYESLNRNV 132
Db 110 EVPTGPLSPQDYDFYSD---AAWYEQETTKGFYSLNTAFDGGTTLAERYDHLINSE 166
QY 133 P-----FIRSSGSRVIASGKKFIEGFOSTKLEKPRAPQGGSSKIDVWISSEASS-----NN 185
Db 167 EKKLSWAGSERVNDTAKYFAGFMKSNYTD-----MVEVJALEEKSQGLS 216
QY 186 TLDPGTCT-----VFEDELADTV---EAFNTATFVPSIRORLENDLSGVTLTDTETVYL 237
Db 217 LTARISCPNYSNHYKDGDFPNDIAERADRLTSP-----GFNTADDP-- 265
QY 238 YMCSPFTTISTVDTKLSFQCLFTHDEMINVDYQSLKKYKYGAGNPLGPTQGVYA 297
Db 266 ALXGFEALVRGE-----SSFCVDLREALLYAYLRDLGWYVNGNPNLGTIGYVYA 320
QY 298 NELIARJTHSPVHDTSSNHTLSSPATFPLSLVLADESHDNGIISILFALGLYNGTK- 356
Db 321 NATROLLENT-----EADPRDYP-----LYFSHSHOTLLQVFTSGCLFNVTSL 364
QY 357 FLSTTTVENTTQDGFSSAKTVFPAGRLYVEMMQC--QAEQEPVLRVLRVNDRVVPVHGCP 414
Db 365 PL-----DQIQFCTSPKSTEIVPMGARLLTERLLCTVEGEKYYVRTLNDVAFPLSDCS 419
QY 415 VDALGRCTRDSFVRGJSFARSGGDWAE 441
Db 420 SGFGFCPCPNJYVSRUEALNEDSDFAE 446

RESULT 12
T39929
Chitin-repressible acid phosphatase - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 33-Dec-1999 #text_change 21-Jan-2000
C:Accession: T39929
Ri:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Xiang, Z.; Aves, S.
submitted to the EMBL Data Library, May 1998
A:Reference number: Z21857
A:Accession: T39929
A:Status: preliminary; translated from GB/EMBL/CDDB
A:Molecule type: DNA
A:Residues: 1-463 <LYN>
A:Cross-references: EMBL:CA01286; PIDN:CA01286.1; GSPDB:GN00067; SPDB:SPB221H7.03c
A:Experimental source: strain 972h-; cosmid c2.1H7
C:Genetics:
A:Gene: SPDB:SPB221H7.03c
A:Map position: 2
C:Superfamily: yeast acid phosphatase

Query Match 12.9%; Score 300; DB 2; Length 463;
Best Local Similarity 26.4%; Pred. No. 3.2e-14;
Matches 108; Conservative 61; Mismatches 180; Indels 60; Gaps 14;

QY 28 YAPFFSLANESVSPVACRVTFQAQLSRHGARYP-----TDSKGGKYSALTEE--- 78
Db 43 HEYFP-----DGLDSAPPETCEQQVHLQRHGSRNPTSDVTA'DVYSQYLNNTQEKLL 97
QY 79 ---IQNATTFDGKFAFLKTYNYSL---GADDLTPFGEQELVNSGKIKFYQRYESLNRNV 132
Db 98 NGSIPNVFSYPENPCJFKQWTEPVIDAENADQLSSRGRLELFDLGRQLCYRYVKLFDYV 157
QY 133 PFISSGSRVIASGKKFIEGFOSTKLEKPRAPQGGSSKIDVWISSEASSNTLDP 189
Db 150 YDINTAEQERWESAKFTYVGFGRNVE-----KTNFILISEGKAAGANSLSMY 207
QY 190 GTCTVDESL-----ADTVENATFATFVPSIRORLENDL-SGVTLTDTETVYLMCMCSP 244
Db 208 NACPVEKDNFNHKNATDAAHVNRN:FIEPIVNRLLAKYFDSSVKLTINDVRSIFYTCEYE 267
QY 245 TISTSTVDTKLSFQCLFTHDEMINVDYQSLKKYKYGAGNPLGPTQGVYANEIARL 304
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Db 268 IAKMHSR-----FCSITPSEFLNFYDSLDGAYGGPVSEWASTJGGAYINKLA--- 319
QY 305 THSPVHEDTSSNHTLSSPATFPLNSTLYADFSHONGIISILFALGLYNGTKPLSTTIVE 364
Db 320 -----DSLNRVT---NP---DFDRKVF-LAFTHDSNLIIPVEAALGFFFDITPQNPPLTD 366
QY 365 NTQDGFSSAWTVFPASRLYVEMMQCAEQEPVLRVLRVNDRVVPVHGC 413
Db 367 KNIYTSOKTSSPFPFAGNLITELFFC-SDSKYYVRHLVNRQVYPLIDC 414

RESULT 13
A25326
acid phosphatase (EC 3.1.3.2) precursor [similarity] - fission yeast (Schizosaccharon
C:Species: Schizosaccharomyces pombe
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: A25326; T50435
Ri:Elliot, S.; Chang, C.; Schweingruber, M.E.; Schaller, J.; Rickli, E.E.; Carbon, J.
J. Biol. Chem. 267, 2936-2941, 1996
A:Title: Isolation and characterization of the structural gene for secreted acid phos
A:Reference number: A25326; MUID:8614050; PMID:3035272
A:Accession: A25326
A:Molecule type: DNA
A:Residues: 1-453 <ELL>
A:Cross-references: GB:M11857; NID:G173422; PIDN:AAA3321.1; PID:G173423
Ri:Rieger, M.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, January 2000
A:Reference number: Z25068
A:Accession: T50435
A:Molecule type: DNA
A:Residues: 1-453 <R13>
A:Cross-references: EMBL:AL137099; PIDN:CB68657.1; GSPDB:GN00067; SPDB:SPB463.12
A:Experimental source: strain 972h(-); clone pl p4G3
C:Genetics:
A:Gene: PHO1; SPDB:SPB24G3.02
A:Map position: 2
C:Superfamily: Yeast acid phosphatase
C:Keywords: phosphohistidine; phosphoprotein; phosphoric monoester hydrolase
F.69/Active site: Arg #status predicted
F.69/Active site: His (phosphohistidine intermediate) #status predicted
```

```
Query Match 12.7%; Score 296.5; DB 1; Length 453;
Best Local Similarity 24.5%; Pred. No. 5.6e-14;
Matches 103; Conservative 57; Mismatches 190; Indels 71; Gaps 12;

QY 18 PSETSHLWQ---YAPFFSLANESVSPV---PACRVTFQAQLSRHGARYPTDSKGGKY 72
Db 30 PDFKEHLTSRSPYHKPYF-----YGPSIDFPTTCKIKQVHT-QRHGSRNPTCGNAAFD 82
QY 73 SALIEEQ-----NATTFDGKFAFLKTYN---YSLGADDLTPFGQELVNSGKIP 120
Db 93 AVGIANFQORLLSGVPIDYVSGNPLSFVPTPTVTEANADALSSGRVELFCMRQF 142
QY 121 YQRYESLNRNVTPFIRSSGSRVIASGKKF-----IEGFOSTKLEKPRAPQGGSSPK 172
Db 143 YERYHELFNASTYNIYTAQQRVVVDSALWYGYGMFGEVDHNFNY1LVSENAAGNS-- 200
QY 173 IDVVISSEASSNNTLDPGCTCTVFEDSELACTVEANFATFVPSIRORLENDLSGVTLTDT 232
Db 201 -----LSSYN-----ACPASDADQFTTPALEARNVYMPPTQRRLNPVFSNYLTND 247
QY 233 EYTVLMDMCSFDTISTTSTVDTKLSFQCLFTHDEMINVDYQSLKKYKYGAGNPLGPTQ 292
Db 248 DILNLYGICVEIALQD-----YSEFCKLFNSVDLFNEFEGLDLSYSGMNSVKGSIF 302
QY 293 GVGVANELLARLTHSPVHCDTSSNHTLSSPATFPLNSTLYADFSHONGIISILFALGLY 352
Db 303 GGAVANSLSLR-----SVENNT-----QQVFFAFTHDANIIIPVEALGFF 344
QY 353 NGTQPLSTTIVENTTQDGFSSAWTVFPASRLYVEMMQCAEQEPVLRVLRVNDRVVPVHGC 412
Db 345 TDNTPENPLPTSYOVHSHMSKASEFVPFAGNLTELPOCE-DSKYYVRHLVNRVNEEVPFLSD 403
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Qy 413 C 413

404 C 404

RESULT: 4

S14119
acid phosphatase (EC 3.1.3.2) - fission yeast (*Schizosaccharomyces pombe*)
C:Species: *Schizosaccharomyces pombe*
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_charge 10-Dec-1993
C:Accession: S14119; T0455
R:Yang, C.; Schweininger, V.E.

Query Match	12.2%	Score 284;	DB 2;	Length 463;
Best Local Similarity	24.9%	Pred. NO. 4.8e-13;		
Matches 102;	Conservative	66;	Mismatches 18;	Indels 60;
Gaps 13;				

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QY      78 --EIQNATTEDGYAFLKTYNSL--GADLTFFGECELVNSGGKFYQRYVESLRNV 132
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QY 133 PIRSSGSRVIAAGKXFIEGFOSTKLKLPRAQFGSSPKDVZ--SEASSNVT.DP :89

190 350VFEDGESL-ADTVEANFIA--TFVPS:RCRJENEL-SGVTJTDTEVTYLNDCSPD 244

QY 245 T:STSTVDTKLSPFCDLFTHEINVDYLOS:KKYVCHGAGNPLGPTQGUYANE:ZARJ 304

QY 305 THISPVHDDTSSNH:LQSSPATFPKNTLYACFSHDNGIISILFALJGYNKTEPLSTTIVE 364

DB 323 R-----KVGNASDRK-----VFLAF-HDSQ-IPVEALGFFPD-----PEHRLPTD 356

QV 365 NITOTDESSANTVPFASGLYVEMMOCAEROERLVRV-LNDRVAPDHGC 413

RESULT 15

A86233

hypothetical protein (imported) - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 24-Aug-2001

C;Accession: A86233
R;heologists, A.; Ecker, J.R.; Paim, C.J.; Federspiel, N.A.; Kaul, S.; White, C.; Alon
Crin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.

Query Match	6.3%	Score 148;	DB 2;	Length 468;
Best Local Similarity	21.8%	Pred. No. 0.0044;		

66 ----DSGKKYSALIEEIQONATTFDGKYAFL-----KTYNVLGADDLTPFGGEQLVNSG 117

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118 IKFYQRYESLTRN-----IVPFRSSGSRVIAHGKKFIEGFSTKGLDPRACPGOSSPKI 173
      .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .

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174 DVVISEASSNNLTDPGCTTVFDS-----ELADTVEANFTATVPVSIRQRLND 223

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:91 FAVTSENRASSD-KLAFEECCQNKYSYRRAKEPAVSKKEPVENK11A-----SVAKRYD-- 244
224 ICSVTLTDTIEVTVYMCMCSFEETISTSTVDTKI SPCFD:ETHDEWINYDYLQSLKRYKYYG 283

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b 245 ---LKFTKQDISSJWFLCKQVALL-----EWTB-----DEVFLKKG 278

279 YGNS:NYKMGV-----PLJEVLHSXEEAIKAREEKLPGSYEKARLRFPAHA 325

326 ET-VPFSCLLGLF.LDGEFEKIOKEKPLEP--PQPPKTRDRFGSTWAPFGNN-LVLYS 383

search completed: November 12, 2003, 14:33:21
 job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw mode:

Run on: November 12, 2003, 14:32:56 ; Search time 33 Seconds
(without alignments)
2310.809 Million cell updates/sec

Title: US-10-062-848-1

Perfect score: 2334

Sequence: 1 ASRQSCDVTQGVQCFSE.....SFVRGLSFARSGGQWAECPA 444

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 3

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications Aa:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	2334	100.0	444	15	US-10-062-848-1
2	2334	100.0	467	15	US-10-079-709-32
3	2334	100.0	467	15	US-10-229-358-5
4	2322	99.5	467	14	US-10-083-452-11
5	2302	98.6	462	15	US-10-229-358-12
6	2259	96.8	467	9	US-09-929-060-3
7	2255	96.6	443	9	US-09-929-060-1
8	2242	96.1	443	9	US-09-929-060-2
9	1971	84.4	410	15	US-10-229-358-11
10	1818	77.9	441	12	US-10-421-122-1
11	1818	77.9	467	14	US-10-083-452-9
12	1699	72.8	467	12	US-10-421-122-2
13	1606.5	68.8	449	15	US-10-062-848-12
14	1606.5	68.8	465	14	US-10-083-452-8
15	1606.5	68.8	465	15	US-10-062-848-78

16	1606.5	68.8	465	15	US-10-229-358-6
17	1606.5	68.8	474	15	US-10-213-930-24
18	1606.5	68.8	439	15	US-10-062-848-3
19	1598.5	68.5	465	15	US-10-062-848-80
20	1597.5	68.4	465	15	US-10-062-848-79
21	1594.5	68.3	465	15	US-10-062-848-81
22	1553.5	66.6	469	15	US-10-062-848-82
23	1532.5	65.7	447	15	US-10-062-848-6
24	1532.5	65.7	463	14	US-10-083-452-10
25	1520	65.1	450	15	US-10-062-848-15
26	1519	65.1	439	15	US-10-062-848-2
27	1513	64.8	489	15	US-10-229-358-4
28	1513	64.8	489	15	US-10-229-358-10
29	1496.5	64.1	450	15	US-10-062-848-9
30	1496.5	64.1	466	14	US-10-083-452-13
31	1493	64.0	466	14	US-10-083-452-12
32	1493	64.0	466	15	US-10-229-358-7
33	1222	52.4	475	14	US-10-083-452-14
34	1215	52.1	355	15	US-10-229-358-15
35	1156	49.5	478	14	US-10-083-452-3
36	1156	49.5	495	14	US-10-083-452-2
37	1129.5	48.4	487	14	US-10-083-452-15
38	1129.5	48.4	487	15	US-10-229-358-8
39	837.5	35.9	284	15	US-10-229-358-19
40	806	34.5	283	15	US-10-229-358-9
41	806	34.5	283	15	US-10-229-358-24
42	762.5	32.7	443	14	US-10-083-452-5
43	762.5	32.7	439	14	US-10-083-452-7
44	735.5	31.7	453	14	US-10-083-452-6
45	732	31.4	442	14	US-10-083-452-4

ALIGNMENTS

RESULT 1
US-10-062-848-1
; Sequence 1, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WISS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,948
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Aspergillus niger
; US-10-062-848-1

Query Match	100.0%	Score 2334	DB 15	Length 444
Best Local Similarity	100.0%	Pred. No. 1.5e-224		
Matches 444	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Cy	1	ASRQSCDVTQGVQCFSESHLWQYAPFFSLANESVISPEVAGCRVTPFQVLSRHG	60	
Db	1	ASRQSCDVTQGVQCFSESHLWQYAPFFSLANESVISPEVAGCRVTPFQVLSRHG	60	
Cy	61	ARYPTDSKGGKYSALIEEQONATTDDGYAFUKTYNYSLGADDLTPFQEQELVNSGIKF	120	
Db	61	ARYPTDSKGGKYSALIEEQONATTDDGYAFUKTYNYSLGADDLTPFQEQELVNSGIKF	120	

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QY 121 YRYESLIRNTPVPIRSGSRVTSAGKKTIEGQSTKLDPRAGQSGSPKIDVWISA 180
DB 121 YRYESLIRNTPVPIRSGSRVTSAGKKTIEGQSTKLDPRAGQSGSPKIDVWISA 180
QY 181 SSSNNTLDPGTCTVFESEADTVEANFTATFVPSIRORLENDLSGVTITDTEVTYLMOM 240
DB 181 SSSNNTLDPGTCTVFESEADTVEANFTATFVPSIRORLENDLSGVTITDTEVTYLMOM 240
QY 241 CSPDTISTSTVDTKLSFPCDLFTHDEMINDYLOSLLKYYGHGAGNPLGFTCGVGYANEL 300
DB 241 CSPDTISTSTVDTKLSFPCDLFTHDEMINDYLOSLLKYYGHGAGNPLGFTCGVGYANEL 300
QY 301 IARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHENGIIISILFALGLVNGTKPLST 360
DB 301 IARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHENGIIISILFALGLVNGTKPLST 360
QY 361 TTVENITQDGFSSAMTVPFASRLYVEMMOCQAEQEPVLRVLVNDRVVPLHGPCVDALGR 420
DB 361 TTVENITQDGFSSAMTVPFASRLYVEMMOCQAEQEPVLRVLVNDRVVPLHGPCVDALGR 420
QY 421 CTRDSFVRGLSFARSGGDWAECPA 444
DB 421 CTRDSFVRGLSFARSGGDWAECPA 444

RESULT 2
US-10-079-709-32
; Sequence 32, Application US/10079709
; Publication No. US20030119163A1
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hattingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Juttin
; APPLICANT: Gerardus Seiten
; TITLE OF INVENTION: Cloning and Expression of Microbia.
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/079,709
; FILING DATE: 32-FEB-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,510
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 07/668,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-10-079-709-32
Query Match 100.0%; Score 2334; DB 15; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.6e-224;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ASRNQSCDVTVDQGYQCFSETSHLWQYAPFFPSLANESVISPEVPAGCRVTFAQVLSRHG 60
DB 24 ASRNQSCDVTVDQGYQCFSETSHLWQYAPFFPSLANESVISPEVPAGCRVTFAQVLSRHG 83
QY 61 ARYPTDSKGKKYSALIEEIQONATTEDGKYAFRLKTYNSLIGADDLTFPGQEQLVNSGIKF 120
DB 84 ARYPTDSKGKKYSALIEEIQONATTEDGKYAFRLKTYNSLIGADDLTFPGQEQLVNSGIKF 143
QY 121 YRYESLIRNTPVPIRSGSRVTSAGKKTIEGQSTKLDPRAGQSGSPKIDVWISA 180
DB 144 YRYESLIRNTPVPIRSGSRVTSAGKKTIEGQSTKLDPRAGQSGSPKIDVWISA 203
QY 181 SSSNNTLDPGTCTVFESEADTVEANFTATFVPSIRORLENDLSGVTITDTEVTYLMOM 240
DB 204 SSSNNTLDPGTCTVFESEADTVEANFTATFVPSIRORLENDLSGVTITDTEVTYLMOM 263
QY 241 CSPDTISTSTVDTKLSFPCDLFTHDEMINDYLOSLLKYYGHGAGNPLGFTCGVGYANEL 300
DB 264 CSPDTISTSTVDTKLSFPCDLFTHDEMINDYLOSLLKYYGHGAGNPLGFTCGVGYANEL 323
QY 301 IARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHENGIIISILFALGLVNGTKPLST 360
DB 324 IARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHENGIIISILFALGLVNGTKPLST 383
QY 361 TTVENITQDGFSSAMTVPFASRLYVEMMOCQAEQEPVLRVLVNDRVVPLHGPCVDALGR 420
DB 384 TTVENITQDGFSSAMTVPFASRLYVEMMOCQAEQEPVLRVLVNDRVVPLHGPCVDALGR 443
QY 421 CTRDSFVRGLSFARSGGDWAECPA 444
DB 444 CTRDSFVRGLSFARSGGDWAECPA 467

RESULT 3
US-10-229-358-5
; Sequence 5, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Trinci, Anthony P.J.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
; FILE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating Same
; FILE REFERENCE: GC586-2
; CURRENT APPLICATION NUMBER: US/10/229,358
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US 60/148,960
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
; US-10-229-358-5
Query Match 100.0%; Score 2334; DB 15; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.6e-224;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ASRNQSCDVTVDQGYQCFSETSHLWQYAPFFPSLANESVISPEVPAGCRVTFAQVLSRHG 60
DB 24 ASRNQSCDVTVDQGYQCFSETSHLWQYAPFFPSLANESVISPEVPAGCRVTFAQVLSRHG 83
QY 61 ARYPTDSKGKKYSALIEEIQONATTEDGKYAFRLKTYNSLIGADDLTFPGQEQLVNSGIKF 120
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84	ARYPTDSCKKYSAJIEI:QCNATTFDKYAFKTYN:SLGADDLTFPGEQELVNSGKF	143
121	YQRYESLSTRNIVPFIIRSSGSRVIAAGKKF:EGFQST:KLDXPRQAQCGQSPKIDVYISEA	180
144	YQRYESLSTRN:VPIIRSSGSRVIAAGKKFIEGFQST:KLDXPRQAQCGQSPKIDVYISEA	203
181	SSNN:LDPGCTTVEDESELADTVEANFTA:TFVPSIRQRLENLSGVTLITDEVTYLMDM	240
204	SSNN:LDPGCTTVEDESELADTVEANFTA:TFVPSIRQRLENLSGVTLITDEVTYLMDM	263
241	CSFDIISTSTVDTKLSPFCDLFTHDEWINYDLSLKKYGHGAGNPLGPTQGVYANEL	300
264	CSFDIISTSTVDTKLSPFCDLFTHDEWINYDLSLKKYGHGAGNPLGPTQGVYANEL	323
301	YARLTHSPVHDTSSNHTLDSPATFPUNSTLYADPFDHNGI:ISLIFALGLYNGTKPUS	360
324	YARLTHSPVHDTSSNHTLDSPATFPUNSTLYADPFDHNGI:ISLIFALGLYNGTKPUS	383
361	TTVEN:TOTDGFSSSAWTVPFASRLYVENMQCQAEPLVRVLVNDRVVP:HGGCFVDALGR	420
384	TTVEN:TOTDGFSSSAWTVPFASRLYVENMQCQAEPLVRVLVNDRVVP:HGGCFVDALGR	443
421	CTRDSFVRGLSPARSGGQWASCEFA	444
444	CTRDSFVRGLSPARSGGQWASCEFA	467

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RESULT: 4
US-10-083-452-11
; Sequence 11, Application: US/10083452
; Publication No. US200201272-8A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Physcane Variants
; FILE REFERENCE: 5618.53C-US
; CURRENT APPLICATION NUMBER: US/10/083,452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273,871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 06407
; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: PA 1998 06206
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-03-18
; PRIOR APPLICATION NUMBER: PA 1999 06091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 6C/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 6C/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 467
; TYPE: PRI
; ORGANISM: Aspergillus ficuum
US-10-083-452-11

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DB      144  YQYESLNRNIVFIRSSGSSRVIASGKFIQFQSTYKDPBAQPSQSPKIDWISIA 203
QY      181  SSSNNLDFGTCVVFQDSSELADVEANFTATVPFSIRQRLNENLDSGVLTCTTEVTYLMDM 240
DB      204  SSSNNLDFGTCVVFQDSSELADVEANFTATVPFSIRQRLNENLDSGVLTCTTEVTYLM 263
QY      241  CSPDTISTSTVDTKLSPPFCDLFTHDWINYCYLCSLKYYGHCAGNPLGPTQGVYANEL 300
DB      264  CSPDTISTSTVDTKLSPPFCDLFTHDWINYCYLCSLKYYGHCAGNPLGPTQGVYANEL 323
QY      301  IARLTHSPVHDDTSSNHTLDSSPATPLKASTLYADFSHNGNIIISILFALGLYNGTKFLST 360
DB      324  IARLTHSPVHDDTSSNHTLDSSPATPLKASTLYADFSHNGNIIISILFALGLYNGTKFLST 383
QY      361  TVVENITCTDGPSSANTVPFASPLVEMMQCAQESPLVRYLVNDRVVPPLGCGVDALGR 420
DB      384  TVVENITCTDGPSSANTVPFASPLVEMMQCAQESPLVRYLVNDRVVPPLGCGVDALGR 443
QY      421  CTRDSFVRGLSFAKSGDMAECPA 444
DB      444  CTRDSFVRGLSFAKSGDMAECPA 467

RESULT 5
US-10-229-358-12
; Sequence 12, Application US/10229358
; Publication NO. US20030124700A1
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Tinci, Anthony P.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids, Encoding
; TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporatin
; FILE REFERENCE: GC586-2
; CURRENT APPLICATION NUMBER: US/10/229,355
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US 60/148,960
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 462
; TYPE: PR1
; ORGANISM: Aspergillus niger
; US-10-229-358-12

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Query Match	98.6%	Score 2302	DB 15	Length 462
Best Local Similarity	99.8%	Pred. No. 2.5e-22		
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Qy 1	ASRNQSSCDTVDGQYOCFSETSLHWGQYAPFFSLANESVISPVPGACRTVTFQVLSRHG	60		
Db 24	ASRNQSSCDTVDGQYOCFSETSLHWGQYAPFFSLANESVISPVPGACRTVTFQVLSRHG	83		
Qy 61	ARYPTDSKGKYGALIEEIQONATTFDGGYAPLKTNYNSLGADDLTPFGQELVNSGIKF	120		
Db 84	ARYPTDSKGKYGALIEEIQONATTFDGGYAPLKTNYNSLGADDLTPFGQELVNSGIKF	143		
Qy 121	YQYESLTRNIVPFIRSSGSSRVIASGKFIEGFQSTKLDKPRAQQSSPKIDVWVISEA	182		
Db 144	YQYESLTRNIVPFIRSSGSSRVIASGKFIEGFQSTKLDKPRAQQSSPKIDVWVISEA	203		
Qy 181	SSSNNTLDPGTCVTFEDELADTVEANFTATVPFSIRORLENLDSGVTLTDTETVYLMDM	240		
Db 204	SSSNNTLDPGTCVTFEDELADTVEANFTATVPFSIRORLENLDSGVTLTDTETVYLMDM	263		
Qy 241	CSPTDISTSVDTKLSPFCDLTFHDEWINVDYLOSLKKYGHGAGNPLGTCQGVYANEL	300		
Db 264	CSPTDISTSVDTKLSPFCDLTFHDEWINVDYLOSLKKYGHGAGNPLGTCQGVYANEL	323		
Qy 301	IARLTHSPVHDDTSNNHTLDSSPATPLNSTLYADFSHCNGIISIFALGLYNGTKPLST	360		

Db 324 IARLTHSPVHDTSSNHTLSSPATFLNSTLYADFSDHNGIISILFALGLYNGTKPLST 383
QY 361 TTVENITQTGFGSSANTVPFASRLYVEMVQCCAEQEPVLRVLVNDRVLPVLRGCPVDALGR 420
Db 384 TTVENITQTGFGSSANTVPFASRLYVEMVQCCAEQEPVLRVLVNDRVLPVLRGCPVDALGR 443
QY 421 CTRDSFVRGLSFARSGGDW 439
Db 444 CTRDSFVRGLSFARSGGDW 462

RESULT 6
US-09-929-060-3
; Sequence 3, Application US/09929060
; Patent No. US20020068350A1
; GENERAL INFORMATION:
; APPLICANT: KONDO, HIEMASA
; APPLICANT: ANAZAWA, HIDEHARU
; APPLICANT: KANEKO, SYUNICHI
; APPLICANT: NAGASHIMA, TADASHI
; APPLICANT: TANGE, TATSUYA
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 081356/0166
; CURRENT APPLICATION NUMBER: US/09/929,060
; CURRENT FILING DATE: 2001-08-05
; PRIOR APPLICATION NUMBER: 09/543,744
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: JP 084114/1996
; PRIOR FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 467
; TYPE: PR1
; ORGANISM: Aspergillus niger
US-09-929-060-3

Query Match 96.8%; Score 2259; DB 9; Length 467;
Best Local Similarity 95.3%; Pred. No. 5.1e-27;
Matches 423; Conservative 14; Mismatches 7; Indels 0; Gaps 0;

QY 1 ASRNQSCDVTVOGQYQCFSETSHLMQYAPFFSLANESVISPEVPACGRVTFAQVLSRHG 60
Db 24 ASRNQSCDVTVOGQYQCFSETSHLMQYAPFFSLANKSAISPDVPAGCHVTFAQVLSRHG 83
QY 61 ARYPTDSKGGKYSALIEEIQONATTEDGKYAFUKTYNSLGADDLTPFGQELVNSGKIF 120
Db 84 ARYPTDSKGGKYSALIEEIQONATTEDGKYAFUKTYNSLGADDLTPFGQELVNSGKIF 143
QY 121 YQYESLTRNIVPFISSGSSSRVIAAGKFTIEGFSQTKLKDPRAQPGQSSPKIDVYVSEA 180
Db 144 YQYESLTRNIVPFISSGSSSRVIAAGKFTIEGFSQTKLKDPRAQPGQSSPKIDVYVSEA 203
QY 181 SSNNTLDPGCTCTVFEDSELADVEANFTATFVPSIRQLENDLSGVTLTDEVTYLMQMC 240
Db 204 STSNNTLDPGCTCTVFEDSELADVEANFTATFVPSIRQLENDLSGVTLTDEVTYLMQMC 263
QY 241 CSFDTISTSTVDTKLSPFCCLFTHDEWINYDYLSKLYKHGAGNPLGPTQGVYANELI 300
Db 264 CSFDTISTSTVDTKLSPFCCLFTHDEWINYDYLSKLYKHGAGNPLGPTQGVYANELI 323
QY 301 IARLTHSPVHDTSSNHTLSSPATFLNSTLYADFSDHNGIISILFALGLYNGTKPLST 360
Db 324 IARLTHSPVHDTSSNHTLSSPATFLNSTLYADFSDHNGIISILFALGLYNGTKPLST 383
QY 361 TTVENITQTGFGSSANTVPFASRLYVEMVQCCAEQEPVLRVLVNDRVLPVLRGCPVDALGR 420
Db 384 TTVENITQTGFGSSANTVPFASRLYVEMVQCCAEQEPVLRVLVNDRVLPVLRGCPVDALGR 443
QY 421 CTRDSFVRGLSFARSGGDW 439

Db 444 CTRDSFVRGLSFARSGGDWGECEFA 467

RESULT 7
US-09-929-060-1
; Sequence 1, Application US/09929060
; Patent No. US20020068350A1
; GENERAL INFORMATION:
; APPLICANT: KONDO, HIEMASA
; APPLICANT: ANAZAWA, HIDEHARU
; APPLICANT: KANEKO, SYUNICHI
; APPLICANT: NAGASHIMA, TADASHI
; APPLICANT: TANGE, TATSUYA
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 081356/0166
; CURRENT APPLICATION NUMBER: US/09/929,060
; CURRENT FILING DATE: 2001-08-05
; PRIOR APPLICATION NUMBER: 09/543,744
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 09/155,855
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: JP 084114/1996
; PRIOR FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 443
; TYPE: PR1
; ORGANISM: Aspergillus niger
US-09-929-060-1

Query Match 96.6%; Score 2255; DB 9; Length 443;
Best Local Similarity 95.3%; Pred. No. 1.2e-216;
Matches 422; Conservative 14; Mismatches 7; Indels 0; Gaps 0;

QY 2 SRNQSCDVTVOGQYQCFSETSHLMQYAPFFSLANESVISPEVPACGRVTFAQVLSRHGA 61
Db 1 SRNQSCDVTVOGQYQCFSETSHLMQYAPFFSLANKSAISPDVPAGCHVTFAQVLSRHGA 60
QY 62 RYPTDSKGGKYSALIEEIQONATTEDGKYAFUKTYNSLGADDLTPFGQELVNSGKIF 121
Db 61 RYPTDSKGGKYSALIEEIQONATTEDGKYAFUKTYNSLGADDLTPFGQELVNSGKIF 120
QY 122 QRYESLTRNIVPFISSGSSSRVIAAGKFTIEGFSQTKLKDPRAQPGQSSPKIDVYVSEA 181
Db 121 QRYESLTRNIVPFISSGSSSRVIAAGKFTIEGFSQTKLKDPRAQPGQSSPKIDVYVSEA 180
QY 182 SSNNTLDPGCTCTVFEDSELADVEANFTATFVPSIRQLENDLSGVTLTDEVTYLMQMC 241
Db 181 SSNNTLDPGCTCTVFEDSELADVEANFTATFVPSIRQLENDLSGVTLTDEVTYLMQMC 240
QY 242 SFDTISTSTVDTKLSPFCCLFTHDEWINYDYLSKLYKHGAGNPLGPTQGVYANELI 301
Db 241 SFDTISTSTVDTKLSPFCCLFTHDEWINYDYLSKLYKHGAGNPLGPTQGVYANELI 300
QY 302 ARLTHSPVHDTSSNHTLSSPATFLNSTLYADFSDHNGIISILFALGLYNGTKPLST 361
Db 301 ARLTHSPVHDTSSNHTLSSPATFLNSTLYADFSDHNGIISILFALGLYNGTKPLST 360
QY 362 TTVENITQTGFGSSANTVPFASRLYVEMVQCCAEQEPVLRVLVNDRVLPVLRGCPVDALGR 421
Db 361 TTVENITQTGFGSSANTVPFASRLYVEMVQCCAEQEPVLRVLVNDRVLPVLRGCPVDALGR 420
QY 422 CTRDSFVRGLSFARSGGDWGECEFA 444
Db 421 CTRDSFVRGLSFARSGGDWGECEFA 443

RESULT 8
US-09-929-060-2
; Sequence 2, Application US/09929060
; Patent No. US20020068350A1
; GENERAL INFORMATION:

```
; APPLICANT: KONDO, HIDEASA
; APPLICANT: AWAZAWA, HIDEHARU
; APPLICANT: KANEKO, SYUNICHI
; APPLICANT: NAGASHIMA, TADASHI
; APPLICANT: TANGE, TATSUYA
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 081356/0166
; CURRENT APPLICATION NUMBER: US/09/329,063
; CURRENT FILING DATE: 2001-08-05
; PRIOR APPLICATION NUMBER: 09/543,744
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 09/155,855
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: JP 0843:4/1996
; PRIOR FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (2)..(3)
; OTHER INFORMATION: Variable Amino Acid
; US-09-929,360-2

Query Match          96.1%; Score 2242; DB 9; Length 443;
Best Local Similarity 94.8%; Pred. No. 2.4e-215;
Matches 420; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 2 SRNCSCTDVQGYOCFSETSHLKGQYAPFFSLANESVISPEVAGCRVTFQAVLSRHGA 61
DB 1 SXNQSTCDTVQGYOCFSETSHLKGQYAPFFSLANESVISPEVAGCRVTFQAVLSRHGA 60
QY 62 RYPTDSKGGKYSALIEEIQONATTFDGKYAFVFLKTYNYSLGADLTPFGEQELVNSGKIF 121
DB 61 RYPTDSKGGKYSALIEEIQONATTFDGKYAFVFLKTYNYSLGADLTPFGEQELVNSGKIF 120
QY 122 QRYESLTRNIVPFRSSGSSRVIASGKXFEIGFQSTKLKDPRAQGGSSPKIDVYISEA 181
DB 121 QRYESLTRNIVPFRSSGSSRVIASGKXFEIGFQSTKLKDPRAQGGSSPKIDVYISEA 180
QY 182 SSNNLTDPGCTCFVDESEADTVFANFTATFVPSIRQRLNDSLVTLTDTETVYLMQW 241
DB 181 TSNNLTDPGCTCFVDESEADTVFANFTATFVPSIRQRLNDSLVTLTDTETVYLMQW 240
QY 242 SPDTISTSTVTKLSPFCOLFTHDEWINDYLSLKYKYGAGNPLGPTQGVYANELI 301
DB 241 SPDTISTSTVTKLSPFCOLFTHDEWINDYLSLKYKYGAGNPLGPTQGVYANELI 300
QY 302 ARLTSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHONGIISILFALGLYNGTKPLST 361
DB 301 ARLTSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHONGIISILFALGLYNGTKPLST 360
QY 362 TVENITQDGFSSAWTVFASRLYVEMMQCQAEQEPFLVRVYVNDRVVPLHGCVPDALGR 421
DB 361 TAENITQDGFSSAWTVFASRLYVEMMQCQAEQEPFLVRVYVNDRVVPLHGCVPDALGR 420
QY 422 TRDSFVRGLSFARSGGDWAECPA 444
DB 421 TRDSFVRGLSFARSGGDWAECPA 443

RESULT 9
US-10-229-358-11
; Sequence 11, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Trinci, Anthony P.J.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
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; TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating Same
; FILE REFERENCE: GC586-2
; CURRENT APPLICATION NUMBER: US/10/229,358
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US 60/148,960
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Aspergillus niger
; US-10-229-358-11

Query Match          84.4%; Score 1971; DB 15; Length 410;
Best Local Similarity 85.9%; Pred. No. 2.7e-188;
Matches 377; Conservative 8; Mismatches 2; Indels 52; Gaps 1;

QY 1 ASNQSCTDVQGYOCFSETSHLKGQYAPFFSLANESVISPEVAGCRVTFQAVLSRHG 60
DB 24 ASNQSCTDVQGYOCFSETSHLKGQYAPFFSLANESVISPEVAGCRVTFQAVLSRHG 59
QY 61 ARYFTDSKGGKYSALIEEIQONATTFDGKYAFVFLKTYNYSLGADLTPFGEQELVNSGKIF 120
DB 84 ARYFTDSKGGKYSALIEEIQONATTFDGKYAFVFLKTYNYSLGADLTPFGEQELVNSGKIF 143
QY 121 QRYESLTRNIVPFRSSGSSRVIASGKXFEIGFQSTKLKDPRAQGGSSPKIDVYISEA 180
DB 144 QRYESLTRNIVPFRSSGSSRVIASGKXFEIGFQSTKLKDPRAQGGSSPKIDVYISEA 203
QY 181 SSNNLTDPGCTCFVDESEADTVFANFTATFVPSIRQRLNDSLVTLTDTETVYLMQW 240
DB 204 SSNNLTDPGCTCFVDESEADTVFANFTATFVPSIRQRLNDSLVTLTDTETVYLMQW 212
QY 241 CSPDTISTSTVTKLSPFCOLFTHDEWINDYLSLKYKYGAGNPLGPTQGVYANELI 300
DB 213 -SPDTISTSTVTKLSPFCOLFTHDEWINDYLSLKYKYGAGNPLGPTQGVYANELI 271
QY 301 IASLTSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHONGIISILFALGLYNGTKPLST 360
DB 272 IASLTSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHONGIISILFALGLYNGTKPLST 331
QY 361 TVENITQDGFSSAWTVFASRLYVEMMQCQAEQEPFLVRVYVNDRVVPLHGCVPDALGR 420
DB 332 TVENITQDGFSSAWTVFASRLYVEMMQCQAEQEPFLVRVYVNDRVVPLHGCVPDALGR 391
QY 421 CTSDSFVRGLSFARSGGDW 439
DB 392 CTSDSFVRGLSFARSGGDW 410

RESULT 10
US-10-421-112-1
; Sequence 1, Application US/10421112
; Publication No. US20030290677A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/10/421,112
; CURRENT FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US/09/634,493A
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US/09/121,425
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: EPO 97112688.3
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Artificial Sequence
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```
;
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
; OTHER INFORMATION: sequence
US-10-421-112-1
```

```
Query Match 77.9%; Score 1818; DB 12; Length 441;
Best Local Similarity 76.6%; Pred. No. 64e-173;
Matches 338; Conservative 39; Mismatches 64; Indels 0; Gaps 0;
```

```
QY 4 NOSCDTVDGGYCCFSETSHLWGOYAPFSSLANESVISEVPAGCRVTFQAVLSRHGARY 63
DB 1 NSHSCDVTDDGYCCFPEISHLWGOYSPYFSEDESALISPDVDDCRVTFVQVLSRHGARY 60
QY 64 PTOSKGGKYKYSALISEICQNAITFDGKYAFUKTYNYSLGADDLTFPGQDELVNSGKIFYQR 123
DB 61 PTSSKSKAYSALLLEAIOKNATAFKGYAFUKTYNYTLGADDLTFPGENQVNSGKIFYRR 120
QY 124 YESLTRNIVPFIRSSGSSRVIASGKFFIEGFSQAKLADPGSQPHQASPVLDVIFEGSGY 193
DB 121 YKALARKIVPFIRASGSDRVIASAEKFFIEGFSQAKLADPGSQPHQASPVLDVIFEGSGY 180
QY 184 NNTLDPGTCTVFEDSELADVEANFTATFVPS*RCQLENDLCSGVTLTDEVTYVMDMCSF 243
DB 181 NNTLDHGTCTAFEDSELGDDVEANFTALFAPARLEADLPGVTLTDEVDVYMDMCPF 240
QY 244 DTISTSTVDTKLSPFCDLFTHDEMIVNDY*QSLKYYVGHGAGNPLGPTQGVGVANELIAR 303
DB 241 ETVARTSDATELSFPCALFTHDEWRQYDY*QSLKYYVGHGAGNPLGPAQGVGFANELIAR 300
QY 304 LTHSPVHDDTSSNHTLDSSEATPPLNSTLYADFSHONGIISILFPA*GLYNGTKPLSTTV 363
DB 301 LTRSPVQDHTSTNHTLDSNPATPPLNATLYADFSHONSMISIFPALGLYNGTAPLSTTSV 360
QY 364 ENITQTQGFSSANTVPFASLYVEMMOCAEQSPLVRLVNDRVLP*HGCPCVDALGRCTR 423
DB 361 ESIBETDGYASNTVPFGARAYVEMMOCAEKSPLVRLVNDRVLP*HGCPCVDALGRCKR 420
QY 424 DSFVRLGSFARSGGDWAECEFA 444
DB 421 DDFVEGLSFARSGGNWAECEFA 441
```

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RESULT 11
US-10-083-452-9
; Sequence 9; Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.50C-US
; CURRENT APPLICATION NUMBER: US/10/083.452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/99/273.871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1996-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080.129
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/090.675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Variation
US-10-083-452-9
```

```
Query Match 77.9%; Score 1818; DB 14; Length 467;
Best Local Similarity 76.6%; Pred. No. 7e-173;
Matches 338; Conservative 39; Mismatches 64; Indels 0; Gaps 0;
```

```
QY 4 NOSCDTVDGGYCCFSETSHLWGOYAPFSSLANESVISEVPAGCRVTFQAVLSRHGARY 63
DB 27 NSHSCDVTDDGYCCFPEISHLWGOYSPYFSEDESALISPDVDDCRVTFVQVLSRHGARY 86
QY 64 PTOSKGGKYKYSALISEICQNAITFDGKYAFUKTYNYSLGADDLTFPGQDELVNSGKIFYQR 123
DB 87 PTSSKSKAYSALLLEAIOKNATAFKGYAFUKTYNYTLGADDLTFPGENQVNSGKIFYRR 146
QY 124 YESLTRNIVPFIRSSGSSRVIASGKFFIEGFSQAKLADPGSQPHQASPVLDVIFEGSGY 206
DB 147 YKALARKIVPFIRASGSDRVIASAEKFFIEGFSQAKLADPGSQPHQASPVLDVIFEGSGY 204
QY 184 NNTLDPGTCTVFEDSELADVEANFTATFVPS*RCQLENDLCSGVTLTDEVTYVMDMCSF 243
DB 207 NNTLDHGTCTAFEDSELGDDVEANFTALFAPARLEADLPGVTLTDEVDVYMDMCPF 266
QY 244 DTISTSTVDTKLSPFCDLFTHDEMIVNDY*QSLKYYVGHGAGNPLGPTQGVGVANELIAR 303
DB 267 ETVARTSDATELSFPCALFTHDEWRQYDY*QSLKYYVGHGAGNPLGPAQGVGFANELIAR 326
QY 304 LTHSPVHDDTSSNHTLDSSEATPPLNSTLYADFSHONGIISILFPA*GLYNGTKPLSTTV 363
DB 327 LTRSPVQDHTSTNHTLDSNPATPPLNATLYADFSHONSMISIFPALGLYNGTAPLSTTSV 386
QY 364 ENITQTQGFSSANTVPFASLYVEMMOCAEQSPLVRLVNDRVLP*HGCPCVDALGRCTR 423
DB 387 ESIBETDGYASNTVPFGARAYVEMMOCAEKSPLVRLVNDRVLP*HGCPCVDALGRCKR 446
QY 424 DSFVRLGSFARSGGDWAECEFA 444
DB 447 DDFVEGLSFARSGGNWAECEFA 467
```

```
RESULT 12
US-10-421-112-2
; Sequence 2; Application US/10421112
; Publication No. US20030190677A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/10/421.112
; CURRENT FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US/09/634.493A
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US/09/121.425
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: EPO 97112688.3
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
; OTHER INFORMATION: sequence
US 10-421-112-2
```

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Query Match 72.8%; Score 1699; DB 12; Length 467;
Best Local Similarity 59.8%; Pred. No. 5.7e-161;
Matches 322; Conservative 38; Mismatches 61; Indels 40; Gaps 2;
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```
QY 4 NOSCDTVDGGYCCFSETSHLWGOYAPFSSLANESVISEVPAGCRVTFQAVLSRHGARY 63
DB 1 NSHSCDVTDDGYCCFPEISHLWGOYSPYFSEDESALISPDVDDCRVTFVQVLSRHGARY 86
QY 64 PTOSKGGKYKYSALISEICQNAITFDGKYAFUKTYNYSLGADDLTFPGQDELVNSGKIFYQR 123
DB 87 PTSSKSKAYSALLLEAIOKNATAFKGYAFUKTYNYTLGADDLTFPGENQVNSGKIFYRR 146
QY 124 YESLTRNIVPFIRSSGSSRVIASGKFFIEGFSQAKLADPGSQPHQASPVLDVIFEGSGY 206
DB 147 YKALARKIVPFIRASGSDRVIASAEKFFIEGFSQAKLADPGSQPHQASPVLDVIFEGSGY 204
QY 184 NNTLDPGTCTVFEDSELADVEANFTATFVPS*RCQLENDLCSGVTLTDEVTYVMDMCSF 243
DB 207 NNTLDHGTCTAFEDSELGDDVEANFTALFAPARLEADLPGVTLTDEVDVYMDMCPF 266
QY 244 DTISTSTVDTKLSPFCDLFTHDEMIVNDY*QSLKYYVGHGAGNPLGPTQGVGVANELIAR 303
DB 267 ETVARTSDATELSFPCALFTHDEWRQYDY*QSLKYYVGHGAGNPLGPAQGVGFANELIAR 326
QY 304 LTHSPVHDDTSSNHTLDSSEATPPLNSTLYADFSHONGIISILFPA*GLYNGTKPLSTTV 363
DB 327 LTRSPVQDHTSTNHTLDSNPATPPLNATLYADFSHONSMISIFPALGLYNGTAPLSTTSV 386
QY 364 ENITQTQGFSSANTVPFASLYVEMMOCAEQSPLVRLVNDRVLP*HGCPCVDALGRCTR 423
DB 387 ESIBETDGYASNTVPFGARAYVEMMOCAEKSPLVRLVNDRVLP*HGCPCVDALGRCKR 446
QY 424 DSFVRLGSFARSGGDWAECEFA 444
DB 447 DDFVEGLSFARSGGNWAECEFA 467
```

```
DE 27 NSHSCDTVDGGYCCPEPESHLWGQSPYFSELESALSPVYDRCRTVFQVLSRHGARY 86
QY 64 PTDSKGYKYSALIEIQONATTFCQYAFJKTNYNSLGADDTLPFGCEGLVNSGKIFYOR 123
DB 97 PTSSKSKAYS-----TNYVTLGADDTLPFGENQMVNSGKIFYR 126
QY 124 YESLTRNVFPIRSGSSRVIASGKKIEGFCSTKLKDPRAQPGQSSPKID----- 174
DB 127 YKALARKVPIRAGSGSRVIAAEKIEGFCSTKLKADPGSCPHQASPVIDLIAQKNA 186
QY 175 -----VWIEASSNNITLDPGCTTVFEDSELADTVAEANFTATVPISIRORLEND 223
DB 187 TAFKGYAFLXVILPEGSGYNNLTHGCTAFEDSELGDDVEANFTALFAIRARLEAD 246
QY 224 LSGVTLTDEVTYLMXCSFTISTSTVDTKLSFPCSLFTHDEMINVYJLSLKKYVGHG 283
DB 247 LPGVTLTDEVDVYLMXCMPEFTVARTSATLSLFPFCAJFTHDEMRQVLDYLSLKKYVYG 306
QY 284 AGNPJGPTQGVYAKNELIARLTHSPVHDTSSNHTLSSSPATFPNSTLYADPFSHNGI 343
DB 307 AGNPJGPAQGVGFANELIARLTHSPVQDHTSNHTLDSKRPATFPNLATLYADPFSHNGI 366
QY 344 SIFALGLYNGTKPLSTTTVENITQDGFSSAWTVPFASRLVEMMCCOAEPLVRLV 403
DB 367 SIFALGLYNGTAPLSTTSVESIBTDGYSASWTVPFCARAYVEMMCCOAEKESLVRVLV 426
QY 404 NDRVPLHGCPVLCALGRTCSFVGLSFARSGGDWAECEFA 444
DB 427 NDRVPLHGCAVCKLGRCKRDEVEGLSFARSGGWNAECEFA 467

RESULT 13
US-10-062-848-12
; Sequence 12, Application US/10062848
; Publication No. US2003092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREMA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 12
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-12

Query Match 68.8%; Score 1606.5; DB 15; Length 449;
Best Local Similarity 66.4%; Pred. No. 9.6e-152;
Matches 295; Conservative 59; Mismatches 89; Indels 1; Gaps 1;

QY 1 ASRNGSSCDTVDOGYOCFSETHLWGQVAPFPLSLANESVISEPVAGCRVTFACVLSRHG 60
DB 7 SAGSKSCDVTDLGYQCSPATSHLWGQSPFSELESVSSKJPKDCRITLVQVLSRHG 66
QY 61 ARYPTDSKGYKYSALIEIQONATTFCQYAFJKTNYNSLGADDTLPFGCEGLVNSGKIF 120
DB 67 ARYPTSSKSKYKLVLTALQANATDFKCKFAFLKTYNTLQADDTLPFGCEGLVNSGKIF 126
QY 121 YORYESLTRNVFPIRSGSSRVIASGKKIEGFCSTKLKDPRAQPGQSSPKIDVYVISEA 180
DB 127 YORYKALARSVVVPIRAGSGSRVIAAEKIEGFCSTKLKADPGATPFAIRARLEAD 186

US-10-062-848-12
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QY 181 SSSNNTLDPGCTTVFEDSELADTVAEANFTATVPISIRORLENDLGSVTLTDEVTYLMX 240
DB 186 ETPNNTLDHGVTCKFEASQGLGDEVAANFTALFAIRARAEKHLPGVTLTDEVDVLSMDM 245
QY 241 CSFDTTSTSTVDTKLSFPCSLFTHDEMINVYJLSLKKYVGHGAGNPLGPTQGVYANEL 300
DB 246 CSFDTVARTSDASQUSFPFCLFTHDEMINVYJLSLKKYVGHGAGNPLGPTQGVYANEL 305
QY 301 IARLTHSPVHDTSSNHTLSSSPATFPNSTLYADPFSHNGIISLFLALGLYNGTKPLST 360
DB 306 IARLTHSPVQDHTSTKSTLVSNPATFPNLATVYVDFSHDNSMVSIFPALGLYNGTEPLSR 365
QY 361 TVVENTITQDGFSSAWTVPFASRLVEMMCCOAEPLVRLVLRVLRVLPJHGPVDAJGR 420
DB 366 TVVESAKELDGYASAGWVPFGARAYFETVQCKSEKEPLVRLALINDRVVPLHGCDDVJGR 425
QY 421 CTRDSFVRSLSPARSGGDWAECEFA 444
DB 426 CRANDFVKLSWARSOGNWECEFS 449

RESULT 14
US-10-083-452-8
; Sequence 8, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618,500-US
; CURRENT APPLICATION NUMBER: US/10/083,452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273,671
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00906
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/050,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-083-452-8

Query Match 68.8%; Score 1606.5; DB 14; Length 465;
Best Local Similarity 66.4%; Pred. No. 1e-151;
Matches 295; Conservative 59; Mismatches 89; Indels 1; Gaps 1;
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QY 1 ASRNGSSCDTVDOGYOCFSETHLWGQVAPFPLSLANESVISEPVAGCRVTFACVLSRHG 60
DB 23 SAGSKSCDVTDLGYQCSPATSHLWGQSPFSELESVSSKJPKDCRITLVQVLSRHG 82
QY 61 ARYPTDSKGYKYSALIEIQONATTFCQYAFJKTNYNSLGADDTLPFGCEGLVNSGKIF 120
DB 83 ARYPTSSKSKYKLVLTALQANATDFKCKFAFLKTYNTLQADDTLPFGCEGLVNSGKIF 142
QY 121 YORYESLTRNVFPIRSGSSRVIASGKKIEGFCSTKLKDPRAQPGQSSPKIDVYVISEA 180
DB 143 YORYKALARSVVVPIRAGSGSRVIAAEKIEGFCSTKLKADPGATPFAIRARLEAD 201
QY 181 SSSNNTLDPGCTTVFEDSELADTVAEANFTATVPISIRORLENDLGSVTLTDEVTYLMX 240
DB 202 ETPNNTLDHGVTCKFEASQGLGDEVAANFTALFAIRARAEKHLPGVTLTDEVDVLSMDM 261
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QY 241 CSFDTISTVDTKLSPFCDLFDHEDWINDYDLSLKKYKGGAGNP-GPTQGYGYANEL 300
 DB 262 CSFDTVARTSDASQSLSPCCQLFTHNKKYNYLQSLKKYGYGAGNP-GPAQGGFTNEL 321
 QY 301 ZARLTHSPVHDTSSNHTLDSSPATFPLNSTLYADFSHNGIIS-LFALGLYNGTKPLST 360
 DB 322 ZARLTRSPVQCHTSTNSTLVSNPATFPLNATVYDFSHKNSVSIFFALGLYNGTEPLSR 381
 QY 361 TTVENITQDTGSSAWTPFASRLYVEMMOCAEQEPLVRVLRVDRVPLHGCPCVALGR 420
 DB 382 TSVESAKELDGYASASWVPFGARAYFETMOCKSEKEPLVRALINDRVVPLHGCPCVALGR 441

QY 421 CTRDSFVRGLSPARSGGDWAECPA 444
 DB 442 CKLNDFFVKGLSWARSGGNWGECPA 465

RESULT 15
 US-10-062-848-78
 : Sequence 78, Application US/0642848
 : Publication No. US20030392155A1
 : GENERAL INFORMATION:
 : APPLICANT: KOSTREWA, Dirk
 : APPLICANT: PASAMONTES, Luis
 : APPLICANT: TOMSCHY, Andrea
 : APPLICANT: van LOON, Adolphus
 : APPLICANT: VOGEL, Kurt
 : APPLICANT: WYSS, Markus
 : TITLE OF INVENTION: MODIFIED PHYTASES
 : FILE REFERENCE: Modified Phytases
 : CURRENT APPLICATION NUMBER: US/0/062.848
 : CURRENT FILING DATE: 2002-02-01
 : PRIOR APPLICATION NUMBER: 09/044.718
 : PRIOR FILING DATE: 1998-03-19
 : PRIOR APPLICATION NUMBER: EP 97810175.6
 : PRIOR FILING DATE: 1997-03-25
 : NUMBER OF SEQ ID NOS: 82
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 78
 : LENGTH: 465
 : TYPE: PRI
 : ORGANISM: Aspergillus fumigatus
 US-10-062-848-78

Query Match 68.8%; Score 1606.5; DB 15; Length 465;
 Best Local Similarity 66.4%; Pred. No. 1e-151;
 Matches 295; Conservative 59; Mismatches 89; Indels 1; Gaps 1;
 QY 1 ASRNOSSCDTVQGYQCFSETSHLMQYAPFFPSLANESVISEVPAGCRVTTAQVLSRHG 60
 DB 23 SSAGSKSCCTVDLGYQCSPATSHLMQYSPFFSEDELVSSSKLPKDCRITLVQVLSRHG 82
 QY 61 ARYPTDSKKKYKALJEEIQONATTFQGYAFUKTYNS:GADDLTPFGCEJYNSG:KF 120
 DB 83 ARYPTSKKKYKALJEEIQONATTFQGYAFUKTYNS:GADDLTPFGCEJYNSG:KF 142
 QY 121 YORYESLTRNVPIFSSSSSRVSIAGSKKFEIGFQSTKLKDFRAQFGSSPKIDVYVISEA 180
 DB 143 YORYKALANSVVFIFRASSGDRVIASGEKEIEGFOQAKLADPGA-TNRAAPALSVIPIPS 201
 QY 181 SSNNITLDPGCTCTFESELSADTVEANFTATFVPSIRQLENLSGVLTDTDEVLYXDM 240
 DB 202 ETFTNTLDHGVCTKFEASQLGDEVAANFTALFAPDIRAPAEKELPGVTJTDDEVSLYDM 261
 QY 241 CSFDTISTVDTKLSPFCDLFDHEDWINDYDLSLKKYKGGAGNP-GPTQGYGYANEL 300
 DB 262 CSFDTVARTSDASQSLSPCCQLFTHNKKYNYLQSLKKYGYGAGNP-GPAQGGFTNEL 321
 QY 301 ZARLTHSPVHDTSSNHTLDSSPATFPLNSTLYADFSHNGIIS-LFALGLYNGTKPLST 360
 DB 322 ZARLTRSPVQCHTSTNSTLVSNPATFPLNATVYDFSHKNSVSIFFALGLYNGTEPLSR 381

QY 361 TTVENITQDTGSSAWTPFASRLYVEMMOCAEQEPLVRVLRVDRVPLHGCPCVALGR 420
 DB 382 TSVESAKELDGYASASWVPFGARAYFETMOCKSEKEPLVRALINDRVVPLHGCPCVALGR 441
 QY 421 CTRDSFVRGLSPARSGGDWAECPA 444
 DB 442 CKLNDFFVKGLSWARSGGNWGECPA 465

Search completed: November 12, 2003, 14:38:19
 Job time : 34 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 12, 2003, 14:30:30 ; Search time 21 Seconds
(without alignments)

894,572 Million: cell updates/sec

Title: US-10-062-848-1
Perfect score: 2334
Sequence: 1 ASRNQSSCDTVQGYQCFSE.....SFRGLSFARSGDWAECFA 444

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/iaa/5A_COVB pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COVB pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB pep.*
5: /cgn2_6/ptodata/1/iaa/FCFUS_COMB pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1 pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2334	100.0	444	4	US-09-044-718-1 Sequence 1, Appl.
2	2334	100.0	467	1	US-08-151-574-32 Sequence 32, App.
3	2334	100.0	467	1	US-08-146-424-20 Sequence 20, App.
4	2334	100.0	467	1	US-08-603-729-2 Sequence 2, Appl.
5	2334	100.0	467	2	US-08-419-448-32 Sequence 32, App.
6	2334	100.0	467	2	US-08-819-825-3 Sequence 3, Appl.
7	2334	100.0	467	3	US-09-163-642-3 Sequence 3, Appl.
8	2334	100.0	467	4	US-09-233-510-32 Sequence 32, Appl.
9	2334	100.0	467	4	US-09-636-499-5 Sequence 5, Appl.
10	2322	99.5	467	4	US-09-273-871A-11 Sequence 11, App.
11	2302	98.6	462	4	US-09-636-493-12 Sequence 12, App.
12	2290	98.1	467	2	US-07-923-724-8 Sequence 8, Appl.
13	2290	98.1	467	2	US-08-609-426A-8 Sequence 8, Appl.
14	2290	98.1	467	3	US-08-374-652C-2 Sequence 2, Appl.
15	2259	96.8	467	3	US-09-155-855-3 Sequence 3, Appl.
16	2259	96.8	467	4	US-09-543-744-3 Sequence 3, Appl.
17	2259	96.8	467	4	US-09-929-060-3 Sequence 3, Appl.
18	2255	96.6	443	3	US-09-155-855-1 Sequence 1, Appl.
19	2255	96.6	443	4	US-09-543-744-1 Sequence 1, Appl.
20	2255	96.6	443	4	US-09-929-060-1 Sequence 1, Appl.
21	2242	96.1	443	3	US-09-155-855-2 Sequence 2, Appl.
22	2242	96.1	443	4	US-09-543-744-2 Sequence 2, Appl.
23	2242	96.1	443	4	US-09-929-060-2 Sequence 2, Appl.
24	1971	84.4	410	4	US-09-636-499-11 Sequence 11, Appl.
25	1818	77.9	441	3	US-09-121-425-1 Sequence 1, Appl.
26	1818	77.9	441	4	US-09-634-493A-1 Sequence 1, Appl.
27	1818	77.9	467	4	US-09-273-871A-9 Sequence 9, Appl.

ALIGNMENTS

RESULT 1
US-09-044-718-1

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; Sequence 1, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: VAN LOON, Adolphus
; APPLICANT: VOGLER, Kurt
; APPLICANT: WISS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044,718
; CURRENT FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 978,0175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Aspergillus niger
; US-09-044-718-1

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Query Match 100.0%; Score 2334; DB 4; Length 444;
Best local Similarity 100.0%; Pred. No. 1.1e-232;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASRNQSSCDTVQGYQCFSESHLWQVAPFSLANESVISPEVAGCRVTPFAVLRSRG 60
    |||||
DB 1 ASRNQSSCDTVQGYQCFSESHLWQVAPFSLANESVISPEVAGCRVTPFAVLRSRG 60
    |||||

QY 61 ARYPFDSKGGKYSALIEEQQNATFDGKYALKNYNSLGGADLTTPGEQLVNSGIKF 120
    |||||
DB 61 ARYPFDSKGGKYSALIEEQQNATFDGKYALKNYNSLGGADLTTPGEQLVNSGIKF 120
    |||||

QY 121 YORYESLTENIYVFFRSGSSSRVSIAGSKKFIEGFSTKLKDPRAOPGQSSPKIDVVISIA 180
    |||||
DB 121 YORYESLTENIYVFFRSGSSSRVSIAGSKKFIEGFSTKLKDPRAOPGQSSPKIDVVISIA 180
    |||||

QY 181 SSSNNLTDPGCTCTVFEDSELADTVEANFTATVPVSIQRLKNDLSGVLTDTDEVTYLMDM 240
    |||||
DB 181 SSSNNLTDPGCTCTVFEDSELADTVEANFTATVPVSIQRLKNDLSGVLTDTDEVTYLMDM 240
    |||||

QY 241 CSFDTISTSTVDTKSPFCDLTHDEWINDYLOSLKKYGHGAGNPLGPTGVGYANEL 300
    |||||
DB 241 CSFDTISTSTVDTKSPFCDLTHDEWINDYLOSLKKYGHGAGNPLGPTGVGYANEL 300
    |||||

QY 301 IARLTHSPVHDDTSSNHTLDDSSPATFELNSTLYADFSDHNGIISILFALGLYNGTKPLST 360
    |||||

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Db 301 IARLTHSPVHDTSSNHTLDSSPATFPLNSTLYADFSHDNGIISLFAALGLYNGTKPST 360
QY 361 TTVENITOTDGFSSAWTVFFASRLYVEMMQCAEQEPJVRVLVNDRVVPLHGGCPVDALGR 420
Db 361 TTVENITOTDGFSSAWTVFFASRLYVEMMQCAEQEPJVRVLVNDRVVPLHGGCPVDALGR 420
QY 421 CTRDSFVRGLSFARSGGDWAECEFA 444
Db 421 CTRDSFVRGLSFARSGGDWAECEFA 444

RESULT 2
US-08-151-574-32
; Sequence 32, Application US/08151574
; Patent No. 5436156
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorpcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veerstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Se'ten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,574
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/698,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-151-574-32

Query Match 100.0%; Score 2334; DB 1; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASRNQSCSDTVDOGYQCFSETSHLWQCYAPFFSLANESVISEVPAGCGRTVFAQVLSRHG 60
Db 24 ASRNQSCSDTVDOGYQCFSETSHLWQCYAPFFSLANESVISEVPAGCGRTVFAQVLSRHG 83
QY 61 ARYPTDSKGGKYSALIEECQNATTFDGKYAFUKTYNYSLGADDTTPFGEQELVNSGKIF 120
Db 84 ARYPTDSKGGKYSALIEECQNATTFDGKYAFUKTYNYSLGADDTTPFGEQELVNSGKIF 143
QY 121 YQRYESLJTRNIVPFISSGSSSRVIASGKRFIEGFQSKLKDPRAPQGQSSPKIDVWISA 180

Db 144 YQRYESLJTRNIVPFISSGSSSRVIASGKRFIEGFQSKLKDPRAPQGQSSPKIDVWISA 203
QY 181 SSNNITLDGTCITVFEDSELAOTVEANFTATFVPS:RORLENDLSGVTLTDTDEVTYLMDX 240
Db 204 SSNNITLDGTCITVFEDSELAOTVEANFTATFVPS:RORLENDLSGVTLTDTDEVTYLMDX 263
QY 241 CSPDTISTSTVTKLSPPCDLFTHDENINYDLOS:KKYKHGAGNPLGPTOGVYANEL 300
Db 264 CSPDTISTSTVTKLSPPCDLFTHDENINYDLOS:KKYKHGAGNPLGPTOGVYANEL 323
QY 301 IARLTHSPVHDTSSNHTLDSSPATFPLNSTLYADFSHDNGIISLFAALGLYNGTKPST 360
Db 324 IARLTHSPVHDTSSNHTLDSSPATFPLNSTLYADFSHDNGIISLFAALGLYNGTKPST 383
QY 361 TTVENITOTDGFSSAWTVFFASRLYVEMMQCAEQEPJVRVLVNDRVVPLHGGCPVDALGR 420
Db 394 TTVENITOTDGFSSAWTVFFASRLYVEMMQCAEQEPJVRVLVNDRVVPLHGGCPVDALGR 443
QY 421 CTRDSFVRGLSFARSGGDWAECEFA 444
Db 444 CTRDSFVRGLSFARSGGDWAECEFA 467

RESULT 3
US-08-146-424-20
; Sequence 20, Application US/08-46424
; Patent No. 5593963
; GENERAL INFORMATION:
; APPLICANT: VAN OOIJEN, ALBERT J. J.
; APPLICANT: RIETVELD, KRIJN
; APPLICANT: HOEKEMA, ANDREAS
; APPLICANT: PEN, JAN
; APPLICANT: S-JMONS, PETER C.
; APPLICANT: VERWOERD, TEUNIS C.
; TITLE OF INVENTION: THE EXPRESSION OF PHYTASE IN PLANTS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,424
; FILING DATE: 02-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KENNEDY, BILL
; REGISTRATION NUMBER: 33,407
; REFERENCE/DOCKET NUMBER: 44615-20011.24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-146-424-20

Query Match 100.0%; Score 2334; DB 1; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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CY 1 ASRNSCCTVDGQYCCFSETSHLMGOYAPFESLANESVISPEVPAGCRVTTACVLSRHG 60
DB 24 ASRNSCCTVDGQYCCFSETSHLMGOYAPFESLANESVISPEVPAGCRVTTACVLSRHG 83
CY 61 ARYPDTSKGGKYSALIEEIQONATTFDGGYAFKTYNSLGGADLTTPGGEQELVNSGKIF 120
DB 84 ARYPDTSKGGKYSALIEEIQONATTFDGGYAFKTYNSLGGADLTTPGGEQELVNSGKIF 143
CY 121 YORYESLTRNIVPFISSGSSRVIASGKKFIEGFQSTKLKOPRAQGGSSPKIDVWVISEA 180
DB 144 YORYESLTRNIVPFISSGSSRVIASGKKFIEGFQSTKLKOPRAQGGSSPKIDVWVISEA 203
CY 181 SSSNNTLDPGCTCTVFEDSELACTVEANFTATVPSSIRQRLENCLSGVTLTDEVTYLMOM 240
DB 204 SSSNNTLDPGCTCTVFEDSELACTVEANFTATVPSSIRQRLENCLSGVTLTDEVTYLMOM 263
CY 241 CSFDTISTSTVDTKLSPPFCDLTFHDEWINDYLSLKKYVGHGAGNPLGPTCGVGYANEL 300
DB 264 CSFDTISTSTVDTKLSPPFCDLTFHDEWINDYLSLKKYVGHGAGNPLGPTCGVGYANEL 323
CY 301 IARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSDHONG--ISILPALGLYNGTKPLST 360
DB 324 IARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSDHONG--ISILPALGLYNGTKPLST 383
CY 361 TTVENITQTDGFSASMTVPFASRLVYEMMCCQAECEPLRVLVNDRVVPJHGCPCVDAJGR 420
DB 384 TTVENITQTDGFSASMTVPFASRLVYEMMCCQAECEPLRVLVNDRVVPJHGCPCVDAJGR 443
CY 421 CTRDSFVRGLSPARSGDWAECPA 444
DB 444 CTRDSFVRGLSPARSGDWAECPA 467

RESULT 4
US-08-693-709-2
; Sequence 2, Application US/08693709
; Patent No. 5770413
; GENERAL INFORMATION:
; APPLICANT: VAN OOIJEN, ALBERT J.J.
; APPLICANT: RIETVELD, KRJUN
; APPLICANT: HOEKEMA, ANDREAS
; APPLICANT: PEN, JAN
; APPLICANT: S.J.MONS, PETER C.
; APPLICANT: VERMORDE, TERNIS C.
; TITLE OF INVENTION: THE EXPRESSION OF PHYTASE
; TITLE OF INVENTION: IN PLANTS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693,709
; FILING DATE: 07-AUG-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146,424
; FILING DATE: 02-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20011.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
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TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Signal Sequence
; LOCATION: 1..23
; OTHER INFORMATION:
; US-08-693-709-2

Query Match: 100.0%; Score 2334; DB 1: Length 467;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 ASRNSCCTVDGQYCCFSETSHLMGOYAPFESLANESVISPEVPAGCRVTTACVLSRHG 60
DB 24 ASRNSCCTVDGQYCCFSETSHLMGOYAPFESLANESVISPEVPAGCRVTTACVLSRHG 83
CY 61 ARYPDTSKGGKYSALIEEIQONATTFDGGYAFKTYNSLGGADLTTPGGEQELVNSGKIF 120
DB 84 ARYPDTSKGGKYSALIEEIQONATTFDGGYAFKTYNSLGGADLTTPGGEQELVNSGKIF 143
CY 121 YORYESLTRNIVPFISSGSSRVIASGKKFIEGFQSTKLKOPRAQGGSSPKIDVWVISEA 180
DB 144 YORYESLTRNIVPFISSGSSRVIASGKKFIEGFQSTKLKOPRAQGGSSPKIDVWVISEA 203
CY 181 SSSNNTLDPGCTCTVFEDSELACTVEANFTATVPSSIRQRLENCLSGVTLTDEVTYLMOM 240
DB 204 SSSNNTLDPGCTCTVFEDSELACTVEANFTATVPSSIRQRLENCLSGVTLTDEVTYLMOM 263
CY 241 CSFDTISTSTVDTKLSPPFCDLTFHDEWINDYLSLKKYVGHGAGNPLGPTCGVGYANEL 300
DB 264 CSFDTISTSTVDTKLSPPFCDLTFHDEWINDYLSLKKYVGHGAGNPLGPTCGVGYANEL 323
CY 301 IARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSDHONG--ISILPALGLYNGTKPLST 360
DB 324 IARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSDHONG--ISILPALGLYNGTKPLST 383
CY 361 TTVENITQTDGFSASMTVPFASRLVYEMMCCQAECEPLRVLVNDRVVPJHGCPCVDAJGR 420
DB 384 TTVENITQTDGFSASMTVPFASRLVYEMMCCQAECEPLRVLVNDRVVPJHGCPCVDAJGR 443
CY 421 CTRDSFVRGLSPARSGDWAECPA 444
DB 444 CTRDSFVRGLSPARSGDWAECPA 467

RESULT 5
US-08-419-448-32
; Sequence 32, Application US/08419448
; Patent No. 5863533
; GENERAL INFORMATION:
; APPLICANT: Robert F.X. Van Gorkom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttir
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006-1888
```

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.2, Version #1.25
 SOFTWARE:
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/419,448
 FILING DATE: 10-APR-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Murashige, Kate H.
 REGISTRATION NUMBER: 23,959
 REFERENCE/DOCKET NUMBER: 24615-20026.10
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-587-1500
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 467 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 US-08-419-448-32

Query Match 100.0%; Score 2334; DB 2; Length 467;
 Best Local Similarity 100.0%; Pred. No. 1.2e-232;
 Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ASRNSCCDTVDCGYQCFSFSTSLWGQYAPFFSLANESVISPVPAGCRVTRAOVLSRHG	60
DB	24	ASRNSCCDTVDCGYQCFSFSTSLWGQYAPFFSLANESVISPVPAGCRVTRAOVLSRHG	93
QY	61	ARYPTDSKGGKYSALIEEIQONATTFDGKYAFILKTYNSLGADDLTPFGQEQLVNSGIXF	120
DB	84	ARYPTDSKGGKYSALIEEIQONATTFDGKYAFILKTYNSLGADDLTPFGQEQLVNSGIXF	143
QY	121	YQVESLTRNIVPIRSGSSSRVIAAGKPIEGFQSTKLKDPRAQGSQSPKIDVWVSEA	180
DB	144	YQVESLTRNIVPIRSGSSSRVIAAGKPIEGFQSTKLKDPRAQGSQSPKIDVWVSEA	203
QY	181	SSSNTLDPGCTVFEDELADTVEANFTATVPISIRORLENDLSGVTLDTEVTYLMDM	240
DB	204	SSSNTLDPGCTVFEDELADTVEANFTATVPISIRORLENDLSGVTLDTEVTYLMDM	263
QY	241	CSFTTISTSTVDTKLSPFCOLFTHDEWINDYQLQSLKKYKHGAGNPLGPTQGVGYANEL	300
DB	264	CSFTTISTSTVDTKLSPFCOLFTHDEWINDYQLQSLKKYKHGAGNPLGPTQGVGYANEL	323
QY	301	IARLTHSPVHDDTSSNHTLDSSPATPLNSTLYADFSHONGIISILFALGLYNGTKPLST	360
DB	324	IARLTHSPVHDDTSSNHTLDSSPATPLNSTLYADFSHONGIISILFALGLYNGTKPLST	383
QY	361	TTVENITQTDGFSASATVPFASRLYVEMMQCAEQEPPLVRVLVNDRVVPLHGCPVDALGR	420
DB	384	TTVENITQTDGFSASATVPFASRLYVEMMQCAEQEPPLVRVLVNDRVVPLHGCPVDALGR	443
QY	421	CTRDSFVRGLSFARSGGDWAECEFA	444
DB	444	CTRDSFVRGLSFARSGGDWAECEFA	467

RESULT 5
 US-08-419-448-32
 ; Sequence 3, Application US/08819625
 ; Patent No. 5866118
 ; GENERAL INFORMATION:
 ; APPLICANT: Berka, Randy M.
 ; APPLICANT: Ray, Michael W.
 ; APPLICANT: Klosz, Alan V.
 ; TITLE OF INVENTION: Polypeptides Having Phytase Activity
 ; TITLE OF INVENTION: And Nucleic Acids Encoding Same
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:

ADDRESSSEE: No. 58661180 No. 5866118disk of No. 5866118th America, Inc.
 STREET: 405 Lexington Avenue, Suite 6400
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10174-6401
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq For Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/619,825
 FILING DATE: 18-MAR-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Lambiris, Elias C.
 REGISTRATION NUMBER: 33,728
 REFERENCE/DOCKET NUMBER: 4758.200-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 867 5123
 TELEFAX: 212 867 0258
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 467 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-619-825-3

Query Match 100.0%; Score 2334; DB 2; Length 467;
 Best Local Similarity 100.0%; Pred. No. 1.2e-232;
 Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ASRNSCCDTVDCGYQCFSFSTSLWGQYAPFFSLANESVISPVPAGCRVTRAOVLSRHG	60
DB	24	ASRNSCCDTVDCGYQCFSFSTSLWGQYAPFFSLANESVISPVPAGCRVTRAOVLSRHG	83
QY	61	ARYPTDSKGGKYSALIEEIQONATTFDGKYAFILKTYNSLGADDLTPFGQEQLVNSGIXF	120
DB	84	ARYPTDSKGGKYSALIEEIQONATTFDGKYAFILKTYNSLGADDLTPFGQEQLVNSGIXF	143
QY	121	YQVESLTRNIVPIRSGSSSRVIAAGKPIEGFQSTKLKDPRAQGSQSPKIDVWVSEA	180
DB	144	YQVESLTRNIVPIRSGSSSRVIAAGKPIEGFQSTKLKDPRAQGSQSPKIDVWVSEA	203
QY	181	SSSNTLDPGCTVFEDELADTVEANFTATVPISIRORLENDLSGVTLDTEVTYLMDM	240
DB	204	SSSNTLDPGCTVFEDELADTVEANFTATVPISIRORLENDLSGVTLDTEVTYLMDM	263
QY	241	CSFTTISTSTVDTKLSPFCOLFTHDEWINDYQLQSLKKYKHGAGNPLGPTQGVGYANEL	300
DB	264	CSFTTISTSTVDTKLSPFCOLFTHDEWINDYQLQSLKKYKHGAGNPLGPTQGVGYANEL	323
QY	301	IARLTHSPVHDDTSSNHTLDSSPATPLNSTLYADFSHONGIISILFALGLYNGTKPLST	360
DB	324	IARLTHSPVHDDTSSNHTLDSSPATPLNSTLYADFSHONGIISILFALGLYNGTKPLST	383
QY	361	TTVENITQTDGFSASATVPFASRLYVEMMQCAEQEPPLVRVLVNDRVVPLHGCPVDALGR	420
DB	384	TTVENITQTDGFSASATVPFASRLYVEMMQCAEQEPPLVRVLVNDRVVPLHGCPVDALGR	443
QY	421	CTRDSFVRGLSFARSGGDWAECEFA	444
DB	444	CTRDSFVRGLSFARSGGDWAECEFA	467

RESULT 7
 US-09-163-842-3
 ; Sequence 3, Application US/09163642
 ; Patent No. 6221644
 ; GENERAL INFORMATION:
 ; APPLICANT: Berka, Randy M.

APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V.
TITLE OF INVENTION: Polypeptides Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: No. 62216440 No. 6221644disk of No. 6221644th America, Inc.
STREET: 405 Lexington Avenue, Suite 640C
City: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/163,642
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/819,825
FILING DATE: 18-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Iambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4758,200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 3298
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-163-642-3

Query Match 100.0%; Score 2334; DB 3; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASRNQSSCTVDQGYOCFSETSHLWQYAPFFSLANESVISPVEPAGCRVTFQAQLSRHG 60
|||||
DB 24 ASRNQSSCTVDQGYOCFSETSHLWQYAPFFSLANESVISPVEPAGCRVTFQAQLSRHG 83
|||||
QY 61 ARYPYDSKGGKYSAL::EEIQONATTFDCKYAFKTYNYSLGADDLTPFGEQELVNSGKIF 120
|||||
DB 84 ARYPYDSKGGKYSAL::EEIQONATTFDCKYAFKTYNYSLGADDLTPFGEQELVNSGKIF 143
|||||
QY 121 YORYESLNRNIVPFRSSGSSRVIASGKKFIEGFQSTKPKDPRACQOSSPKIDWVISEA 180
|||||
DB 144 YORYESLNRNIVPFRSSGSSRVIASGKKFIEGFQSTKPKDPRACQOSSPKIDWVISEA 203
|||||
QY 181 SSSNNLDPGCTCTVPEDSELADTVEANFTATVPISIRORLENDLSGVTLTDTEVTYLMDM 240
|||||
DB 204 SSSNNLDPGCTCTVPEDSELADTVEANFTATVPISIRORLENDLSGVTLTDTEVTYLMDM 263
|||||
QY 241 CSFDTISTSTVDTKLSPFCDLFTHOEWINYDLSKYYKHGAGNPLGTQGVGYANEL 300
|||||
DB 264 CSFDTISTSTVDTKLSPFCDLFTHOEWINYDLSKYYKHGAGNPLGTQGVGYANEL 323
|||||
QY 301 IARLTHSPVHDDTSNHTLDSPPATFP::NSTLYADFSHDNGIIISILFALGLYNGTKPLST 360
|||||
DB 324 IARLTHSPVHDDTSNHTLDSPPATFP::NSTLYADFSHDNGIIISILFALGLYNGTKPLST 383
|||||
QY 361 TTVENITC'DGPFSSAWTVFASRLVEMMQOAEPLVRVLRVNDRVVPLHGCVPDALGR 420
|||||
DB 384 TTVENITC'DGPFSSAWTVFASRLVEMMQOAEPLVRVLRVNDRVVPLHGCVPDALGR 443
|||||
QY 421 CTRDSFVRGLSFARSGGDWAECPA 444
|||||

DB 444 CTRDSFVRGLSFARSGGDWAECPA 467

RESULT 8
US-09-233-510-32
Sequence 32, Application US/09233510
Patent No. 630602
GENERAL INFORMATION:
APPLICANT: Robert F.M. Van Gorcom
APPLICANT: Willem Van Hartingsveldt
APPLICANT: Petrus A. Van Paridon
APPLICANT: Annemarie E. Veenstra
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Gerardus Seiden
TITLE OF INVENTION: Cloning and Expression of Microbial
TITLE OF INVENTION: Phytase
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
City: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025-3471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,510
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/688,578
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20026.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
TELEFAX: 415-327-2951
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-233-510-32

Query Match 100.0%; Score 2334; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASRNQSSCTVDQGYOCFSETSHLWQYAPFFSLANESVISPVEPAGCRVTFQAQLSRHG 60
|||||
DB 24 ASRNQSSCTVDQGYOCFSETSHLWQYAPFFSLANESVISPVEPAGCRVTFQAQLSRHG 83
|||||
QY 61 ARYPYDSKGGKYSALIEETQONATTFDCKYAFKTYNYSLGADDLTPFGEQELVNSGKIF 120
|||||
DB 84 ARYPYDSKGGKYSALIEETQONATTFDCKYAFKTYNYSLGADDLTPFGEQELVNSGKIF 143
|||||
QY 121 YORYESLNRNIVPFRSSGSSRVIASGKKFIEGFQSTKPKDPRACQOSSPKIDWVISEA 180
|||||
DB 144 YORYESLNRNIVPFRSSGSSRVIASGKKFIEGFQSTKPKDPRACQOSSPKIDWVISEA 203
|||||
QY 181 SSSNNLDPGCTCTVPEDSELADTVEANFTATVPISIRORLENDLSGVTLTDTEVTYLMDM 240
|||||
DB 204 SSSNNLDPGCTCTVPEDSELADTVEANFTATVPISIRORLENDLSGVTLTDTEVTYLMDM 263
|||||
QY 241 CSFDTISTSTVDTKLSPFCDLFTHOEWINYDLSKYYKHGAGNPLGTQGVGYANEL 300
|||||

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Db 264 CSFDTISTVDTKLSFCDLTHDEWYNDYLSKYYGSGAGNPLGPTQGVYANEL 323
QY 301 IARLTHSPVHDDTSSNHTLDSSPATPPKNTSLYADFSDHNGIISILFALGLYNGTKPLST 360
Db 324 IARLTHSPVHDDTSSNHTLDSSPATPPKNTSLYADFSDHNGIISILFALGLYNGTKPLST 383
QY 361 TTVENITQTDGSSAWTVPFASRLYVEMMCCOAEQPLVRVLVNDRVVPLHGCPCVDALGR 420
Db 384 TTVENITQTDGSSAWTVPFASRLYVEMMCCOAEQPLVRVLVNDRVVPLHGCPCVDALGR 443
QY 421 CTRDSFVRGLSFARSGGDWAECPA 444
Db 444 CTRDSFVRGLSFARSGGDWAECPA 467

RESULT 9
US-09-636-499-5
; Sequence 5, Application US/09636499
; Patent No. 6475762
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Trinci, Anthony P.J.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
; FILE REFERENCE: GC586-2
; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/148,960
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 5
; LENGTH: 467
; TYPE: PR1
; ORGANISM: Aspergillus niger
US-09-636-499-5

Query Match 100.0%; Score 2334; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASRNQSSCDTVQGYOCFSETSHLWQYAPFFSLANESVISPEVPAGCRVTPAQVLSRHG 60
Db 24 ASRNQSSCDTVQGYOCFSETSHLWQYAPFFSLANESVISPEVPAGCRVTPAQVLSRHG 83
QY 61 ARYPTDSKGGKYSALIEEIQONATTFDGKYAFKTYNYSLSGADDLTPGQELVNSGKIF 120
Db 84 ARYPTDSKGGKYSALIEEIQONATTFDGKYAFKTYNYSLSGADDLTPGQELVNSGKIF 143
QY 121 YQYESLTRNIVPFISSGSSRVIASGKKFIEGFQSTKLDPRAGQSSPKIDVYISEA 180
Db 144 YQYESLTRNIVPFISSGSSRVIASGKKFIEGFQSTKLDPRAGQSSPKIDVYISEA 203
QY 181 SSSNNTLDPGTCTVFEDESADTVEANFTATVPFSIRQLENDLSGVTLTDEVTYMDM 240
Db 204 SSSNNTLDPGTCTVFEDESADTVEANFTATVPFSIRQLENDLSGVTLTDEVTYMDM 263
QY 241 CSFDTISTVDTKLSFCDLTHDEWYNDYLSKYYGSGAGNPLGPTQGVYANEL 300
Db 264 CSFDTISTVDTKLSFCDLTHDEWYNDYLSKYYGSGAGNPLGPTQGVYANEL 323
QY 301 IARLTHSPVHDDTSSNHTLDSSPATPPKNTSLYADFSDHNGIISILFALGLYNGTKPLST 360
Db 324 IARLTHSPVHDDTSSNHTLDSSPATPPKNTSLYADFSDHNGIISILFALGLYNGTKPLST 383
QY 361 TTVENITQTDGSSAWTVPFASRLYVEMMCCOAEQPLVRVLVNDRVVPLHGCPCVDALGR 420
Db 384 TTVENITQTDGSSAWTVPFASRLYVEMMCCOAEQPLVRVLVNDRVVPLHGCPCVDALGR 443
QY 421 CTRDSFVRGLSFARSGGDWAECPA 444

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Db 444 CTRDSFVRGLSFARSGGDWAECPA 467

RESULT 10
US-09-273-871A-11
; Sequence 11, Application US/09273871A
; Patent No. 6514495
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.50C-JS
; CURRENT APPLICATION NUMBER: US/09/273,871A
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 11
; LENGTH: 467
; TYPE: PR1
; ORGANISM: Aspergillus ficuim
US-09-273-871A-11

Query Match 99.5%; Score 2322; DB 4; Length 467;
Best Local Similarity 99.5%; Pred. No. 2.1e-231;
Matches 442; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASRNQSSCDTVQGYOCFSETSHLWQYAPFFSLANESVISPEVPAGCRVTPAQVLSRHG 60
Db 24 ASRNQSSCDTVQGYOCFSETSHLWQYAPFFSLANESVISPEVPAGCRVTPAQVLSRHG 83
QY 61 ARYPTDSKGGKYSALIEEIQONATTFDGKYAFKTYNYSLSGADDLTPGQELVNSGKIF 120
Db 84 ARYPTDSKGGKYSALIEEIQONATTFDGKYAFKTYNYSLSGADDLTPGQELVNSGKIF 143
QY 121 YQYESLTRNIVPFISSGSSRVIASGKKFIEGFQSTKLDPRAGQSSPKIDVYISEA 180
Db 144 YQYESLTRNIVPFISSGSSRVIASGKKFIEGFQSTKLDPRAGQSSPKIDVYISEA 203
QY 181 SSSNNTLDPGTCTVFEDESADTVEANFTATVPFSIRQLENDLSGVTLTDEVTYMDM 240
Db 204 SSSNNTLDPGTCTVFEDESADTVEANFTATVPFSIRQLENDLSGVTLTDEVTYMDM 263
QY 241 CSFDTISTVDTKLSFCDLTHDEWYNDYLSKYYGSGAGNPLGPTQGVYANEL 300
Db 264 CSFDTISTVDTKLSFCDLTHDEWYNDYLSKYYGSGAGNPLGPTQGVYANEL 323
QY 301 IARLTHSPVHDDTSSNHTLDSSPATPPKNTSLYADFSDHNGIISILFALGLYNGTKPLST 360
Db 324 IARLTHSPVHDDTSSNHTLDSSPATPPKNTSLYADFSDHNGIISILFALGLYNGTKPLST 383
QY 361 TTVENITQTDGSSAWTVPFASRLYVEMMCCOAEQPLVRVLVNDRVVPLHGCPCVDALGR 420
Db 384 TTVENITQTDGSSAWTVPFASRLYVEMMCCOAEQPLVRVLVNDRVVPLHGCPCVDALGR 443
QY 421 CTRDSFVRGLSFARSGGDWAECPA 444
Db 444 CTRDSFVRGLSFARSGGDWAECPA 467

RESULT 11
US-09-636-499-12
; Sequence 12, Application US/09636499

```

Patent No. 6475762
GENERAL INFORMATION:
APPLICANT: Stafford, Christian F.
APPLICANT: Trinci, Anthony P.J.
APPLICANT: Brookman, Jayne L.
TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating Same
FILE REFERENCE: G586-2
CURRENT APPLICATION NUMBER: US/99/636,499
CURRENT FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: US 60/148,960
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 462
TYPE: PRT
ORGANISM: Aspergillus niger
US-09-636-499-12

Query Match 98.6%; Score 2302; DB 4; Length 462;
Best Local Similarity 99.8%; Pred. No. 2.4e-229;
Matches 438; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASRNOSSCDTVDQGYCCFSESHLWQYAPFSLANESVISPEVPAGCRVTFAQVLSRHG 60
DB 24 ASRNOSSCDTVDQGYCCFSESHLWQYAPFSLANESVISPEVPAGCRVTFAQVLSRHG 83
QY 61 ARYPDSKGGKYSALIEIQNATTFDQKYAFLKTYNYSJGADDLTPFGEQELVNSGIKF 120
DB 84 ARYPDSKGGKYSALIEIQNATTFDQKYAFLKTYNYSJGADDLTPFGEQELVNSGIKF 143
QY 121 YORYESLTRNIVPFIIRSSGSRVZASGKKFIEGPOSTKLKDPRAQPGQSSPKIDWISEA 180
DB 144 YORYESLTRNIVPFIIRSSGSRVZASGKKFIEGPOSTKLKDPRAQPGQSSPKIDWISEA 203
QY 181 SSSNNTLPDGTCTVPEDESELDATVEANFTATFVSIRORLENDLSGVTLTDTVTYLMDM 240
DB 204 SSSNNTLPDGTCTVPEDESELDATVEANFTATFVSIRORLENDLSGVTLTDTVTYLMDM 263
QY 241 CSFDTISTSTVDTKLSPFCDLFTHDEWINDYDLSKKYKHGAGNFIPTQGGVYANEL 300
DB 264 CSFDTISTSTVDTKLSPFCDLFTHDEWINDYDLSKKYKHGAGNFIPTQGGVYANEL 323
QY 301 IARLTHSPVHDDTSSNHTLDSPTATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLST 360
DB 324 IARLTHSPVHDDTSSNHTLDSPTATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLST 383
QY 361 TVVENITQDGFSSAWTVPFASRLYVENMQCAOEPLRVLVNDRVVPJHGPCVDALGR 420
DB 384 TVVENITQDGFSSAWTVPFASRLYVENMQCAOEPLRVLVNDRVVPJHGPCVDALGR 443

RESULT 12
US-C7-923-724-8
Sequence 8, Application US/C7923724
Patent No. 5780292
GENERAL INFORMATION:
APPLICANT: Nevalainen, Helena K.M.
APPLICANT: Paloheimo, Maria T.
APPLICANT: Mattinen-Oinonen, Arja S.K.
APPLICANT: Torkkeli, Tuula K.
APPLICANT: Cantrell, Michael
APPLICANT: Fiddington, Christopher S.
APPLICANT: Rambosek, John A.
APPLICANT: Turunen, Maria K.
APPLICANT: Fagerström, Richard B.
TITLE OF INVENTION: Production of Phytase Degrading Enzymes
TITLE OF INVENTION: in Trichoderma

NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
City: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,724
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 8610600
FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0240004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-923-724-8

Query Match 98.1%; Score 2290; DB 1; Length 467;
Best Local Similarity 97.3%; Pred. No. 4.2e-228;
Matches 432; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASRNOSSCDTVDQGYCCFSESHLWQYAPFSLANESVISPEVPAGCRVTFAQVLSRHG 60
DB 24 ASRNOSSCDTVDQGYCCFSESHLWQYAPFSLANESVISPEVPAGCRVTFAQVLSRHG 83
QY 61 ARYPDSKGGKYSALIEIQNATTFDQKYAFLKTYNYSJGADDLTPFGEQELVNSGIKF 120
DB 84 ARYPDSKGGKYSALIEIQNATTFDQKYAFLKTYNYSJGADDLTPFGEQELVNSGIKF 143
QY 121 YORYESLTRNIVPFIIRSSGSRVZASGKKFIEGPOSTKLKDPRAQPGQSSPKIDWISEA 180
DB 144 YORYESLTRNIVPFIIRSSGSRVZASGKKFIEGPOSTKLKDPRAQPGQSSPKIDWISEA 203
QY 181 SSSNNTLPDGTCTVPEDESELDATVEANFTATFVSIRORLENDLSGVTLTDTVTYLMDM 240
DB 204 SSSNNTLPDGTCTVPEDESELDATVEANFTATFVSIRORLENDLSGVTLTDTVTYLMDM 263
QY 241 CSFDTISTSTVDTKLSPFCDLFTHDEWINDYDLSKKYKHGAGNFIPTQGGVYANEL 300
DB 264 CSFDTISTSTVDTKLSPFCDLFTHDEWINDYDLSKKYKHGAGNFIPTQGGVYANEL 323
QY 301 IARLTHSPVHDDTSSNHTLDSPTATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLST 360
DB 324 IARLTHSPVHDDTSSNHTLDSPTATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLST 383
QY 361 TVVENITQDGFSSAWTVPFASRLYVENMQCAOEPLRVLVNDRVVPJHGPCVDALGR 420
DB 384 TVVENITQDGFSSAWTVPFASRLYVENMQCAOEPLRVLVNDRVVPJHGPCVDALGR 443

QY 421 CTRDSFVRGJSFARSGGDWAECSA 444
DB 444 CTRDSFVRGJSFARSGGDWAECSA 467

US-08-609-426A-8
Sequence 8, Application US/08609426A
Patent No. 583733

GENERAL INFORMATION:
APPLICANT: Nevalainen, Helena K.M.
APPLICANT: Paloheimo, Marja T.
APPLICANT: Miettinen-Oinonen, Arja S.K.
APPLICANT: Torkkeli, Tuula K.
APPLICANT: Cantrell, Michael
APPLICANT: Piddington, Christopher S.
APPLICANT: Rambosek, John A.
APPLICANT: Turunen, Marja K.
APPLICANT: Fagerström, Richard B.
APPLICANT: Houston, Christine S.
TITLE OF INVENTION: Production of Phytase Degrading Enzymes
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1103 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,426A
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/923,724
FILING DATE: 31-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 8610600
FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Grant B.
REGISTRATION NUMBER: P-41,264
REFERENCE/DOCKET NUMBER: 1050.0080001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-609-426A-8

Query Match 98.1%; Score 2290; DB 2: Length 457;
Best Local Similarity 97.3%; Pred. No. 4,2e-226;
Matches 432; Conservative 8; Mismatches 4; Indels 0;

QY 1 ASRNSCCTVDGOCFSTSLWQYAPFFSLANESVISPVPAGCRVTAQVLSRHG 60
DB 24 ASRNSCCTVDGOCFSTSLWQYAPFFSLANESVISPVPAGCRVTAQVLSRHG 83

QY 61 ARYPTSGKKYKYSALIEEIQONATTFDGYAFKTYNYSJGADLTTPGQELVNSGKIF 120
DB 84 ARYPTSGKKYKYSALIEEIQONATTFDGYAFKTYNYSJGADLTTPGQELVNSGKIF 143
QY 121 YORYESLTRNIVPFISSGSSRVIASGKKFIEGPOSTKLKOPRAGPGSSPKIDVWVISA 180
DB 144 YORYESLTRNIVPFISSGSSRVIASGKKFIEGPOSTKLKOPRAGPGSSPKIDVWVISA 203
QY 181 SSSNTLDPGTCTVPEDESEADTVEANFTATFVPSIRQRLNDSGLVTLTDTETVYLMQM 240
DB 204 SSSNTLDPGTCTVPEDESEADTVEANFTATFVPSIRQRLNDSGLVTLTDTETVYLMQM 263
QY 241 CSPDTISTSTVDTKLSPFCOLETHDEWNYDYLOSLKYYGHGAGNPGLPTOGVYANEL 300
DB 264 CSPDTISTSTVDTKLSPFCOLETHDEWNYDYLOSLKYYGHGAGNPGLPTOGVYANEL 323
QY 301 IARLTHSPVEDDTSSNHTLDDSPFATPPPLNSTLYADFSHDNGIISILFALGLYNGTKPLST 360
DB 324 IARLTHSPVEDDTSSNHTLDDSPFATPPPLNSTLYADFSHDNGIISILFALGLYNGTKPLST 383
QY 361 TTVENITQTDGSSAMTVFASRLYVEMMQCAEQSPPLVRVLVNDRVVPLHSCFVDALOR 420
DB 384 TTVENITQTDGSSAMTVFASRLYVEMMQCAEQSPPLVRVLVNDRVVPLHSCFVDALOR 443
QY 421 CTRDSFVRGJSFARSGGDWAECSA 444
DB 444 CTRDSFVRGJSFARSGGDWAECSA 467

RESULT 14
US-06-374-652C-2
Sequence 2, Application US/28374652C
Patent No. 5834286

GENERAL INFORMATION:
APPLICANT: NEVALAINEN, HELENA K.M.
APPLICANT: PALOHEIMO, MARJA T.
APPLICANT: FAGERSTROM, RICHARD B.
APPLICANT: MIETTINEN-OINONEN, ARJA S.
APPLICANT: TURUNEN, MARJA K.
APPLICANT: RAMBOSEK, JOHN A.
APPLICANT: PIDDINGTON, CHRISTOPHER S.
APPLICANT: HOUSTON, CHRISTINE S.
APPLICANT: CANTRELL, MICHAEL A.
TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,
TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTASE DEGRADING
TITLE OF INVENTION: ENZYMES IN DESIRED RATIOS
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.C.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,652C
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07058
FILING DATE: 27-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/925,401
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

```

; NAME: REED, GRANT B.
; REGISTRATION NUMBER: 41,264
; REFERENCE/DOCKET NUMBER: 1050.071001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amaro acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; US-38-374-652C-2

Query Match 98.1%; Score 2280; DB 2; Length 467;
Best Local Similarity 97.3%; Pred. No. 4.2e-228;
Matches 432; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASRNSCSDTVDOGYQCFSETSHLWGQYAPFFSLANESVISEVPAGCRVTFAQVLSRHG 60
DB 24 ASRNSCTDVTDOGYQCFSETSHLWGQYAPFFSLANESVISEVPAGCRVTFAQVLSRHG 83
QY 61 ARYPTDSKGGKYSALIEECCQNTTTFDGKYAFILKTYNSLGGADLTPFGCEQLVNSGKIF 120
DB 84 ARYPTDSKGGKYSALIEECCQNTTTFDGKYAFILKTYNSLGGADLTPFGCEQLVNSGKIF 143
QY 121 YQRYESLTRNIVPFISSGSSSRVIAAGKXPIEGFQSTKLKDPRAQPGQSSPKIDVWVSEA 180
DB 144 YQRYESLTRNIVPFISSGSSSRVIAAGKXPIEGFQSTKLKDPRAQPGQSSPKIDVWVSEA 203
QY 181 SSSNNTLDPGCTVFEQSELADTVEANFTATFVPSIRQRLNDLSGVTLTDTFVTVLMDM 240
DB 204 SSSNNTLDPGCTVFEQSELADTVEANFTATFVPSIRQRLNDLSGVTLTDTFVTVLMDM 263
QY 241 CSFDTISTSTVDTKLSPPFCCLFTHDEWINDYLOS-KKYYGHCAGNPLGPTCGVGYANEL 300
DB 264 CSFDTISTSTVDTKLSPPFCCLFTHDEWINDYLOS-KKYYGHCAGNPLGPTCGVGYANEL 323
QY 301 IARLTHSPVHDDTSSNHTLDSNPATFLNSTLYADPSSHNGIISILFALGLYNGTKPLST 360
DB 324 IARLTHSPVHDDTSSNHTLDSNPATFLNSTLYADPSSHNGIISILFALGLYNGTKPLST 383
QY 361 TTVENITQDGFSSAWTVFPASRLYVEMMQCAEQEPLVAVLVNDRVVPLHSCPDALGR 420
DB 384 TTVENITQDGFSSAWTVFPASRLYVEMMQCAEQEPLVAVLVNDRVVPLHSCPDALGR 443
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DB 444 CTRDSFVRGLSFARSGGDWAECPA 467

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RESULT 15
US-09-155-855-3
; Sequence 3, Application: US/09155855
; Patent No. 6139902
; GENERAL INFORMATION:
; APPLICANT: KONDO, Hiemasa
; APPLICANT: ANAZAWA, Hiemaru
; APPLICANT: KANEKO, Syunichi
; APPLICANT: NAGASHIWA, Tadashi
; APPLICANT: TANGE, Tatsuya
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 61356/124
; CURRENT APPLICATION NUMBER: US/09/155,855
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
; EARLIER FILING DATE: 1997-04-04
; EARLIER APPLICATION NUMBER: JP 084314
; EARLIER FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3

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; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
; US-09-155-855-3

Query Match 96.8%; Score 2259; DB 3; Length 467;
Best Local Similarity 95.3%; Pred. No. 6.8e-225;
Matches 423; Conservative 14; Mismatches 7; Indels 0; Gaps 0;

QY 1 ASRNSCSDTVDOGYQCFSETSHLWGQYAPFFSLANESVISEVPAGCRVTFAQVLSRHG 60
DB 24 ASRNSCTDVTDOGYQCFSETSHLWGQYAPFFSLANESVISEVPAGCRVTFAQVLSRHG 83
QY 61 ARYPTDSKGGKYSALIEECCQNTTTFDGKYAFILKTYNSLGGADLTPFGCEQLVNSGKIF 120
DB 84 ARYPTDSKGGKYSALIEECCQNTTTFDGKYAFILKTYNSLGGADLTPFGCEQLVNSGKIF 143
QY 121 YQRYESLTRNIVPFISSGSSSRVIAAGKXPIEGFQSTKLKDPRAQPGQSSPKIDVWVSEA 180
DB 144 YQRYESLTRNIVPFISSGSSSRVIAAGKXPIEGFQSTKLKDPRAQPGQSSPKIDVWVSEA 203
QY 181 SSSNNTLDPGCTVFEQSELADTVEANFTATFVPSIRQRLNDLSGVTLTDTFVTVLMDM 240
DB 204 SSSNNTLDPGCTVFEQSELADTVEANFTATFVPSIRQRLNDLSGVTLTDTFVTVLMDM 263
QY 241 CSFDTISTSTVDTKLSPPFCCLFTHDEWINDYLOS-KKYYGHCAGNPLGPTCGVGYANEL 300
DB 264 CSFDTISTSTVDTKLSPPFCCLFTHDEWINDYLOS-KKYYGHCAGNPLGPTCGVGYANEL 323
QY 301 IARLTHSPVHDDTSSNHTLDSNPATFLNSTLYADPSSHNGIISILFALGLYNGTKPLST 360
DB 324 IARLTHSPVHDDTSSNHTLDSNPATFLNSTLYADPSSHNGIISILFALGLYNGTKPLST 383
QY 361 TTVENITQDGFSSAWTVFPASRLYVEMMQCAEQEPLVAVLVNDRVVPLHSCPDALGR 420
DB 384 TTVENITQDGFSSAWTVFPASRLYVEMMQCAEQEPLVAVLVNDRVVPLHSCPDALGR 443
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DB 444 CTRDSFVRGLSFARSGGDWAECPA 467

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Search completed: November 12, 2003, 14:33:54
Job time : 22 secs

GenCore version 5.1.6
Copyright: (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw mode.

Run on: November 12, 2003, 14:25:45 : Search time 46 Seconds
(without alignments)
1532.056 Million cell updates/sec

Title: US-10-062-848-1

Perfect score: 2334

Sequence: 1 ASRNQSSCDTVQGVOCFSE.....SFVRGLSPARSGDWACFA 444

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2334	100.0	448	23	ABE83911 Aspergillus niger
2	2334	100.0	449	22	AAV69547 Aspergillus niger
3	2334	100.0	467	12	AA11333 Recombinant chromo
4	2334	100.0	467	18	AAW15124 Aspergillus ficuum
5	2334	100.0	467	20	AAV39904 A. ficuum phytase
6	2334	100.0	467	23	ABE83910 Aspergillus niger
7	2334	100.0	482	22	AAV72978 Carrot extensin le
8	2322	99.5	467	12	AA113360 Phytase, Aspergil
9	2321	99.4	441	21	AA20505 Aspergillus niger

19	2321	99.4	441	21	AAV69548 Aspergillus niger
20	2291	98.2	441	21	AAV69547 Aspergillus niger
21	2290	98.1	467	15	AA46752 Phytase, Aspergil
22	2290	98.1	467	15	AA46752 A. niger phytase
23	2290	98.1	467	15	AA46752 A. niger phytase
24	2278	98.0	441	21	AA20504 Aspergillus niger
25	2277	97.6	441	21	AA20503 Aspergillus niger
26	2277	97.6	441	21	AAV69546 Aspergillus niger
27	2253	96.5	449	22	AAV72973 Aspergillus niger
28	2253	96.5	482	22	AAV72977 Carrot extensin le
29	2252	96.5	467	16	AAW36500 Aspergillus niger
30	1932	82.8	467	20	AAV43172 Consensus phytase
31	1932	82.8	467	21	AAV69571 Phytase-7, a deriv
32	1932	82.8	467	22	AAU02113 Consensus phytase
33	1929	82.6	467	21	AA20529 Consensus phytase
34	1833	78.5	457	20	AAV43169 Consensus phytase
35	1833	78.5	467	21	AA20526 Consensus phytase
36	1833	78.5	467	21	AAV69568 Mutant Phytase-1
37	1833	78.5	467	22	AAU02110 Consensus phytase
38	1828	78.3	467	21	AA20531 Consensus phytase
39	1826	78.2	467	22	AAU03005 Consensus phytase
40	1826	78.2	467	22	AAU03017 Consensus phytase
41	1825	78.2	467	22	AAU03004 Consensus phytase
42	1825	78.2	467	22	AAU03010 Consensus phytase
43	1824	78.1	467	22	AAU03007 Consensus phytase
44	1824	78.1	467	22	AAU03009 Consensus phytase
45	1824	78.1	467	22	AAU03019 Consensus phytase
46	1824	78.1	467	22	AAU03023 Consensus phytase
47	1824	78.1	467	22	AAU03025 Consensus phytase
48	1823	78.1	467	22	AAU03011 Consensus phytase
49	1823	78.1	467	22	AAU03012 Consensus phytase
50	1823	78.1	467	22	AAU03013 Consensus phytase
51	1822	78.1	467	21	AA20532 Consensus phytase
52	1822	78.1	467	22	AAU03003 Consensus phytase
53	1822	78.1	467	22	AAU03008 Consensus phytase
54	1822	78.1	467	22	AAU03027 Consensus phytase
55	1822	78.1	467	22	AAU03028 Consensus phytase

ALIGNMENTS

RESULT :

ABE83911

10 ABE83911: standard; Protein: 448 AA.

AC ABE83911:

XX

XX

XX 17-SEP-2002 (first entry)

XX

XX Aspergillus niger phyA related polypeptide 2.

XX

XX Yeast; Aspergillus niger; phytase; phyA; Pasteur Pichia; enzyme.

XX

XX Aspergillus niger.

XX

XX CN133363-A.

XX

XX 30-JAN-2002.

XX

XX 12-JUL-2000; 2000CN-0117245.

XX

XX 12-JUL-2000; 2000CN-0117245.

XX

XX (RAIS-) INST RAISE LIVESTOCK GUANGDONG ACAD AGRI.

XX

XX Chen Z, Yang L, Fang L;

XX

XX WPI: 2002-305615/35.

XX

XX N-PSDB; ABN85590.

XX

XX Phytase gene sequence and application in yeast thereof -

XX

XX Disclosure; Fig 4; 48pp; Chinese.

PS

XX The invention relates to a coded phytase gene sequence suitable for
CC secretion and expression in yeast and its application. It is mainly
CC characterised by removing nucleotide sequence of +45-+146 bit from phyA
CC total length structure gene sequence, removing Aspergillus niger signal
CC peptide coded sequence of +1-+44 and +147-+159, connecting a part of
CC signal peptide code sequence suitable for secretion and expression at 5'
CC end and connecting a restriction endonuclease site at 3' end. The
CC different carriers can be connected into said gene sequence so as to form
CC a recombinant plasmid with different functions and after the recombinant
CC plasmid using pPICZ alpha A as carrier is converted into Pasteur Pichia
CC yeast, finally the invented Pasteur Pichia yeast engineering bacterium
CC (CCACC NC:M20005) can be obtained through the screening process.
CC By using the invention the industrial process of phytase bio-expression
CC can be successfully implemented. The present sequence is that of a
CC polypeptide of the invention.
XX
SQ Sequence 448 AA;

Query Match 100.0%; Score 2334; DB 23; Length 448;
Best Local Similarity 100.0%; Pred. NC. 2.4e-214;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASRNSCCTVDGQYCFSETSHLMQYAPFFSLANESVISPVEAGCRVTFACVLSRHG 50
DB 5 ASRNSCCTVDGQYCFSETSHLMQYAPFFSLANESVISPVEAGCRVTFACVLSRHG 64
QY 61 ARYPTDSKGGKYSALIEEIQONATTFDGKYAFKTYNYSLGADLTTPFGQELVNSGKIF 120
DB 65 ARYPTDSKGGKYSALIEEIQONATTFDGKYAFKTYNYSLGADLTTPFGQELVNSGKIF 124
QY 121 YQRYESLTRNIVPFISSGSSRVIASGKFIQSTKLDPRAGQSSPKIDVWISA 180
DB 125 YQRYESLTRNIVPFISSGSSRVIASGKFIQSTKLDPRAGQSSPKIDVWISA 184
QY 181 SSSNNTLDPGTCTVFEDSELADTVANFTATFVPSIRQRLENLDSGVTLTDETVYLMDM 240
DB 185 SSSNNTLDPGTCTVFEDSELADTVANFTATFVPSIRQRLENLDSGVTLTDETVYLMDM 244
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DB 365 TTVENITQTDGFSASNTVFPASRLYVEMMCOQAEQEPVVRVLNDRVPLHGCPCVDALGR 424
QY 421 CTRDSFVRGLSFARSGGDWAECEFA 444
DB 425 CTRDSFVRGLSFARSGGDWAECEFA 448

RESULT 2
AA72974
ID AA72974 standard; Protein: 449 AA.
XX
AC AA72974;
XX
XX
DT 13-JUN-2001 (first entry)
XX
DE Aspergillus niger phytase (Phy) A-1 protein.
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KW Phytase A; Phy: plant productivity; phosphorus utility;
KW biomass production; hypocotyl production; epicotyl production;
KW transgenic plant; phytate.
XX
OS Aspergillus niger.
XX
PN WO200122806-A1.

XX 05-APR-2001.
XX
XX 22-SEP-2000; 2000CWO-AU01193.
XX
XX 24-SEP-1999; 99AU-0003049.
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XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX (AUMC) AUSTRALIAN WOOL RES & PROMOTION ORG.
XX
XX Richardson AE, Hayes JE, Simpson RJ;
XX WP7; 2001-244964/25.
XX R-FSD3; AAD03283.
XX
XX New isolated nucleic acid encoding a mature phytase polypeptide for
XX enhancing the phosphorus nutrition of a plant, the growth of a plant on
XX a phosphorus source and the phosphorus content of a plant -
XX
XX Claim 6; Page 124-126; 144pp; English.
XX
XX The invention relates to a method of modifying plant productivity
XX which involves expressing (Phy) A phytase gene from Aspergillus niger,
XX in a plant cell. Phytase gene is capable of facilitating plants
XX ability to utilise soil phosphorus. It is used to enhance the
XX phosphorus nutrition of a plant or the growth of a plant on a
XX phosphorus source comprising phytate and/or increase the
XX phosphorus content of a plant. This gene is used to enhance
XX the biomass produced by a plant and also to enhance the rate
XX of hypocotyl production of the rate of epicotyl production.
XX Transgenic plant containing phytase gene has improved productivity
XX than its isogenic counterparts.
XX The present sequence is Aspergillus niger Phy A-1 protein.
XX
SQ Sequence 449 AA;

Query Match 100.0%; Score 2334; DB 22; Length 449;
Best Local Similarity 100.0%; Pred. NC. 2.5e-214;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASRNSCCTVDGQYCFSETSHLMQYAPFFSLANESVISPVEAGCRVTFACVLSRHG 60
DB 6 ASRNSCCTVDGQYCFSETSHLMQYAPFFSLANESVISPVEAGCRVTFACVLSRHG 65
QY 61 ARYPTDSKGGKYSALIEEIQONATTFDGKYAFKTYNYSLGADLTTPFGQELVNSGKIF 120
DB 66 ARYPTDSKGGKYSALIEEIQONATTFDGKYAFKTYNYSLGADLTTPFGQELVNSGKIF 125
QY 121 YQRYESLTRNIVPFISSGSSRVIASGKFIQSTKLDPRAGQSSPKIDVWISA 180
DB 126 YQRYESLTRNIVPFISSGSSRVIASGKFIQSTKLDPRAGQSSPKIDVWISA 185
QY 181 SSSNNTLDPGTCTVFEDSELADTVANFTATFVPSIRQRLENLDSGVTLTDETVYLMDM 240
DB 186 SSSNNTLDPGTCTVFEDSELADTVANFTATFVPSIRQRLENLDSGVTLTDETVYLMDM 245
QY 241 CSPDTTSTVDTKLSPPFCDLFTHDEWINYDYQLSLKKYVGHGAGNPLGFTQGVGYNEL 300
DB 246 CSPDTTSTVDTKLSPPFCDLFTHDEWINYDYQLSLKKYVGHGAGNPLGFTQGVGYNEL 305
QY 301 IARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLST 360
DB 306 IARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLST 365
QY 361 TTVENITQTDGFSASNTVFPASRLYVEMMCOQAEQEPVVRVLNDRVPLHGCPCVDALGR 420
DB 366 TTVENITQTDGFSASNTVFPASRLYVEMMCOQAEQEPVVRVLNDRVPLHGCPCVDALGR 425
QY 421 CTRDSFVRGLSFARSGGDWAECEFA 444
DB 426 CTRDSFVRGLSFARSGGDWAECEFA 449

```

RESULT 3
AAR11333
ID AAR11333 standard; Protein: 467 AA.
XX
AC AAR11333;
XX
DT 25-MAR-2003 (updated)
DT 30-MAR-2000 (revised)
DT 31-MAY-1991 (first entry)
XX
DE Recombinant chromosomal phytase.
XX
KW Microbial phytase; animal feeds; inositol; inorganic phosphates.
XX
OS synthetic.
XX
PN EP420358-A.
XX
PD 03-APR-1991.
XX
PF 27-SEP-1990; 90EP-0202565.
XX
PR 17-AUG-1990; 90EP-020231.
XX
PR 27-SEP-1989; 89EP-0202436.
XX
PR 27-SEP-1990; 90EP-0202565.
XX
XX (KCNH) GIST-BROCADES NV.
PA (STAM) DSM NV.
XX
PI Van Gorcom RF, Van Hartingsveldt W, Vangariden PA, Beenstra AE;
PI Luiten RG, Sellen GCM;
XX
WP1: 1991-095799/14.
XX
CR N-PSDB; AA011175.
XX
XX
PT DNA encoding phytase - used for recombinant expression for production
PT of phytase for conversion of phytate to inositol and inorganic
PT phosphate esp. in animal feed
XX
PS Disclosure: Fig 8; filpp; English.
XX
XX
CC This sequence is encoded by a DNA sequence deduced from comparisons of
CC respective sequences of clones identified using oligonucleotide probes.
CC The use of recombinant DNA methods for the the enzyme prodn allows the
CC large scale prodn. of proteins and peptides having phytase activity.
CC These are used for the conversion of phytate to inositol and inorganic
CC phosphate and can be used in industrial processes. The phosphate content
CC of manure thus can be decreased. See also AA011157-74.
CC (Revised record issued to correct errors present in the sequence
CC portion of the original GENESEQ entry.)
CC (Updated on 25-MAR-2003 to correct PA field.)
CC (Updated on 23-MAR-2003 to correct PT field.)
XX
SQ Sequence 467 AA;
Query Match 100.0%; Score 2334; DB 12; Length 467;
Best Local Similarity 100.0%; Pred. No. 2,6e-24;
Matches 444; Conservative 0; Mismatches 0; Indels 3; Gaps 0;
QY 1 ASRNGSSCCTVDCGYOCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFPAQVLSRHG 60
Db 24 ASRNGSSCCTVDCGYOCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFPAQVLSRHG 83
QY 61 ARYPDTSKKKYSALTEEBEQNATTFDGGYAFELKTYNLSLGLADDTLPGEQELVNSG:KF 120
Db 94 ARYPDTSKKKYSALTEEBEQNATTFDGGYAFELKTYNLSLGLADDTLPGEQELVNSG:KF 143
QY 121 YQRYESLJTRNIVPFFIRSSGSSRVIASGKXFIQGFSTK:KOPRACPGGSSPKIDVW:SEA 180
Db 144 YQRYESLJTRNIVPFFIRSSGSSRVIASGKXFIQGFSTK:KOPRACPGGSSPKIDVW:SEA 203
QY 181 SSSNNTLDFGCTCTVDFEDELADTVANFTATFVPSIRQRLNDLSGVTLTDTTEVTYMDM 240

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RESULT 4

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AAM15124
ID AAM15124 standard; Protein: 467 AA.
XX
AC AAM15124;
XX
DT 25-MAR-2003 (updated)
DT 21-AUG-1997 (first entry)
XX
DE Aspergillus ficuum phytase.
XX
KW Phytase; phytate; inositol; animal feed.
XX
OS Aspergillus ficuum NRRL 3135.
XX
XX Key Location/Qualifiers
XX Peptide 1..23 /label= Sig_peptide
XX
PN EP779037-A1.
XX
PT 18-JUN-1997.
XX
PR 27-SEP-1990; 96EP-0202943.
XX
PR 27-SEP-1989; 89EP-0202436.
XX
PR 17-AUG-1990; 90EP-020231.
XX
PR 27-SEP-1990; 90EP-0202565.
XX
XX (KCNH) GIST-BROCADES NV.
XX (STAM) DSM NV.
XX
PI Van Paridon PA, Veenstra AE, Luiten RG, Sellen GCM;
PI Van Gorcom RFM, Van Hartingsveldt W;
XX
WP1: 1997-312513/29.
XX
N-PSDB; AAT65136, AAT65137.
XX
Fungal phytase - releases inorganic phosphate from myo-inositol
phosphate, useful to prepare animal feed and reduce phytate levels
in manure
XX
PS Example 8; Fig 8; filpp; English.
XX
CC Aspergillus ficuum phytase (AAM15124) catalyses the conversion of
CC phytate to inositol and inorganic phosphate. It shows optimum
CC activity at pH 5.5 and 2.5, has a specific activity of about 100
CC U/mg and a mol.wt. of 85 kDa (56.5 kDa unglycosylated). Its amino
CC acid sequence was deduced from an isolated phytase cDNA clone
CC (AAT65136). Isolation of this clone allows large-scale prodn. of the
CC phytase in transformed host cells and used to prepare animal feed,
CC reduce phytase levels in manure (by adding the enzyme to animal
CC feed), and also to liberate inorganic phosphates from myo-inositol
CC phosphates in e.g. starch prodn. from cereals and soy processing.

```

CC (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX

SQ Sequence 467 AA;

Query Match: 100.0%; Score 2334; DB 18; Length: 467;
 Best Local Similarity 100.0%; Pred. No. 2.6e-214;
 Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASRQSSCDTVGQYCFSETSHLWQYAPFFSLANESVSEVPAGCRVFAQVLSRHG 60
 DB 24 ASRQSSCDTVGQYCFSETSHLWQYAPFFSLANESVSEVPAGCRVFAQVLSRHG 93
 QY 61 ARYPTDSKGGKYSALIEECQNATTFDGKYAFUKTYNYSLGADLTTPGECELVNSGKIF 120
 DB 84 ARYPTDSKGGKYSALIEECQNATTFDGKYAFUKTYNYSLGADLTTPGECELVNSGKIF 143
 QY 121 YORYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKOPRAQFGOSSPKIDWVISEA 180
 DB 144 YORYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKOPRAQFGOSSPKIDWVISEA 203
 QY 181 SSSNNTLDPGTCTVFEDESLEADTVEANFTATFVPSRQRLNDLSGVTLDTEVTYMDM 240
 DB 204 SSSNNTLDPGTCTVFEDESLEADTVEANFTATFVPSRQRLNDLSGVTLDTEVTYMDM 263
 QY 241 CSFDTISTSTVDTKLSPPFCDLTFHDEWINDYLSKYYGSHGAGNPLGFCGGVYANEL 300
 DB 264 CSFDTISTSTVDTKLSPPFCDLTFHDEWINDYLSKYYGSHGAGNPLGFCGGVYANEL 323
 QY 301 IARLTHSPVHDDTSSNHTLDSPPATFPPLNSTLYADFSHDNGIISILFALGLYNGTKPLST 360
 DB 324 IARLTHSPVHDDTSSNHTLDSPPATFPPLNSTLYADFSHDNGIISILFALGLYNGTKPLST 383
 QY 361 TTVENITQTDGFSASMTVPFASRLYVEMMCCOAEQEPPLVRVLVNDRVVPLHGCPCVDALGR 420
 DB 384 TTVENITQTDGFSASMTVPFASRLYVEMMCCOAEQEPPLVRVLVNDRVVPLHGCPCVDALGR 443
 QY 421 CTRDSFVRGLSFARSGGDWAECPA 444
 DB 444 CTRDSFVRGLSFARSGGDWAECPA 467

RESULT 5
 ID AAY39904
 AC
 AC AAY39904;
 DT 07-DEC-1999 (first entry)
 XX
 DE A. ficum phytase protein sequence.
 XX
 KW Phytase; variant; enzyme; phosphorus liberation; phytase substrate;
 KW Phytate level reduction; animal manure; food preparation;
 KW Soy processing; inositol manufacture.
 XX
 OS Aspergillus ficum.
 XX
 PN WC9549022-A1.
 XX
 PD 30-SEP-1999.
 XX
 PF 22-MAR-1999; 99NO-DK00153.
 XX
 PR 23-MAR-1998; 98DK-00004C7.
 PR 19-JUN-1998; 98DK-00008C6.
 PR 18-SEP-1998; 98DK-0001176.
 PR 22-JAN-1999; 99DK-0000091.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX

PI Svendsen A;
 XX WP; 1999-580444/49.
 DR N-PSDB; AAZ27421.
 XX
 PT New variant phytase enzymes, used for liberating phosphorus from a
 PT phytase substrate, for reducing phytate levels in animal manure and in
 PT feed and food preparations -
 XX
 XX Claim 19; Fig 11; 141pp; English.

CC This sequence represents the Aspergillus ficum phytase sequence.
 CC The invention relates to variant phytase enzymes with specific amino acid
 CC substitutions for improved properties. The phytase variants can be used
 CC for liberating phosphorus from a phytase substrate. They can be used for
 CC reducing phytate levels in animal manure. They can be used in feed or
 CC food preparations. The phytase DNA can also be used to produce transgenic
 CC plants which can be used in feeds or foods. The phytase variants can also
 CC be used in soy processing and in the manufacture of inositol or
 CC derivatives. The phytase variants can have altered activities such as pH
 CC stability, temperature stability, pH profile, temperature profile,
 CC specific activity (in particular in relation to pH and temperature),
 CC substrate specificity, substrate cleavage pattern, substrate binding,
 CC position specificity, the velocity and level of release of phosphate,
 CC from corn, reaction rate, phytase degradation rate and end level of
 CC released phosphate reached.
 XX

SQ Sequence 467 AA;
 Query Match: 100.0%; Score 2334; DB 20; Length 467;
 Best Local Similarity 100.0%; Pred. No. 2.6e-214;
 Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASRQSSCDTVGQYCFSETSHLWQYAPFFSLANESVSEVPAGCRVFAQVLSRHG 60
 DB 24 ASRQSSCDTVGQYCFSETSHLWQYAPFFSLANESVSEVPAGCRVFAQVLSRHG 83
 QY 61 ARYPTDSKGGKYSALIEECQNATTFDGKYAFUKTYNYSLGADLTTPGECELVNSGKIF 120
 DB 84 ARYPTDSKGGKYSALIEECQNATTFDGKYAFUKTYNYSLGADLTTPGECELVNSGKIF 143
 QY 121 YORYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKOPRAQFGOSSPKIDWVISEA 180
 DB 144 YORYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKOPRAQFGOSSPKIDWVISEA 203
 QY 181 SSSNNTLDPGTCTVFEDESLEADTVEANFTATFVPSRQRLNDLSGVTLDTEVTYMDM 240
 DB 204 SSSNNTLDPGTCTVFEDESLEADTVEANFTATFVPSRQRLNDLSGVTLDTEVTYMDM 263
 QY 241 CSFDTISTSTVDTKLSPPFCDLTFHDEWINDYLSKYYGSHGAGNPLGTCGGVYANEL 300
 DB 264 CSFDTISTSTVDTKLSPPFCDLTFHDEWINDYLSKYYGSHGAGNPLGTCGGVYANEL 323
 QY 301 IARLTHSPVHDDTSSNHTLDSPPATFPPLNSTLYADFSHDNGIISILFALGLYNGTKPLST 360
 DB 324 IARLTHSPVHDDTSSNHTLDSPPATFPPLNSTLYADFSHDNGIISILFALGLYNGTKPLST 383
 QY 361 TTVENITQTDGFSASMTVPFASRLYVEMMCCOAEQEPPLVRVLVNDRVVPLHGCPCVDALGR 420
 DB 384 TTVENITQTDGFSASMTVPFASRLYVEMMCCOAEQEPPLVRVLVNDRVVPLHGCPCVDALGR 443
 QY 421 CTRDSFVRGLSFARSGGDWAECPA 444
 DB 444 CTRDSFVRGLSFARSGGDWAECPA 467

RESULT 6
 ID ABB83810
 AC ABB83810;
 XX
 XX ABB83810;
 DT 17-SEP-2002 (first entry)

XX Aspergillus niger phyA related polypeptide i.
XX Yeast: Aspergillus niger; phytase; phyA; Pasteur Pichia; enzyme.
XX Aspergillus niger.
XX CN1333363-A.
XX 30-CAN-2002.
XX 12-JUL-2000; 2000CN-0117245.
XX 12-JUL-2000; 2000CN-0117245.
XX (RAIS-) INST RAISE LIVESTOCK GUANGDONG ACAD AGRI.
XX Chen Z, Yang L, Fang L;
XX WPI; 2002-305615/35.
XX N-PSDB; ABN85588.
XX Phytase gene sequence and application in yeast thereof -
XX Disclosure; Fig 2; 48pp; Chinese.
XX The invention relates to a coded phytase gene sequence suitable for
XX secretion and expression in yeast and its application. It is mainly
XX characterised by removing nucleotide sequence of +45..146 bit from phyA
XX total length structure gene sequence, removing Aspergillus niger signal
XX peptide coded sequence of +1..44 and +147..159, connecting a part of
XX signal peptide code sequence suitable for secretion and expression at 5'
XX end and connecting a restriction endonuclease site at 3' end, the
XX different carriers can be connected into said gene sequence so as to form
XX a recombinant plasmid with different functions and after the recombinant
XX plasmid using pPICZ alpha A as carrier is converted into Pasteur Pichia
XX yeast, finally the invented Pasteur Pichia yeast engineering bacterium
XX (CCTCC NO.W200005) can be obtained through the screening process.
XX By using the invention the industrial process of phytase bio-expression
XX can be successfully implemented. The present sequence is that of a
XX polypeptide of the invention.
XX Sequence 467 AA;
XX Query Match 100.0%; Score 2334; DB 23; Length 467;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-214;
XX Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ASRNCSSCDTVDOGGYQCFSE*SHLWGOYAPFPFSLANESV*SPVEPAGCRVTFACVLSPHG 60
CH 24 ASRNCSSCDTVDOGGYQCFSE*SHLWGOYAPFPFSLANESV*SPVEPAGCRVTFACVLSPHG 83
QY 61 ARYPTDSKXKYSALIEIEIQONATTFDGKYAF*LTNYNSLGGADLTTPFGQELVNSG*KF 120
DB 84 ARYPTDSKXKYSALIEIEIQONATTFDGKYAF*LTNYNSLGGADLTTPFGQELVNSG*KF 143
QY 121 YORYESLARNIVPFRSSSSRVIASGKKFIEGFQSTK*KKPRACPGOSSPKIDVWVISEA 180
DB 144 YORYESLARNIVPFRSSSSRVIASGKKFIEGFQSTK*KKPRACPGOSSPKIDVWVISEA 203
QY 181 SSSNNTLDPGTCTVDESELAOTVEANFTATVPRIORLENDLSGVTLTDEVTYLMCM 240
DB 204 SSSNNTLDPGTCTVDESELAOTVEANFTATVPRIORLENDLSGVTLTDEVTYLMCM 263
QY 241 CSFDTISTSTVDTKUSPFCDLJTHDEWINYDLSLKKYXGAGNPLGPTGGVGYANEL 300
DB 264 CSFDTISTSTVDTKUSPFCDLJTHDEWINYDLSLKKYXGAGNPLGPTGGVGYANEL 323
QY 301 IARLTHSPVHDTSSNHTLDSSPATFPNLSLYADFSDHNGIISILFALGLYNGTKPLST 360
DB 324 IARLTHSPVHDTSSNHTLDSSPATFPNLSLYADFSDHNGIISILFALGLYNGTKPLST 383
QY 361 TTVENITQDTGFSSAWTVPFASRLYVENMQCAEGEPLVRVLVNDVRVPLHGCPVDALGR 420

DB 334 TTVENITQDTGFSSAWTVPFASRLYVENMQCAEGEPLVRVLVNDVRVPLHGCPVDALGR 443
QY 421 CTGDSFVRLGSLSPARSGGWAECEFA 444
DB 444 CTGDSFVRLGSLSPARSGGWAECEFA 467
RESULT 7
AAV72978
ID AAV72978 standard; Protein; 482 AA.
XX AAV72978;
AC AAV72978;
XX 13-JUN-2001 (first entry)
XX Carrot extensin leader peptide-A. niger phytase A-1 chimeric protein.
XX Phytase A: Phy; plant productivity; phosphorus utility;
XX biomass production; hypocotyl production; epicotyl production;
XX transgenic plant; phytate; carrot; extensin.
XX Chimeric - Daucus carota.
XX Chimeric - Aspergillus niger.
XX Key Location/Qualifiers
XX Peptide 1..33
XX Protein 34..482
XX /label= Mature carrot extensin leader peptide-
XX A. niger phytase A-2 Chimeric protein
XX WO200122806-A1.
XX C5-APR-2001.
XX 22-SEP-2000; 2000WC-AU01163.
XX 24-SEP-1999; 99AU-0003049.
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX (AUWC-) AUSTRALIAN WOOL RES & PROMOTION ORG.
XX Richardson AE, Hayes JE, Simpson RJ;
XX WPI; 2001-244964/25.
XX N-PSDB; AADC3287.
XX New isolated nucleic acid encoding a mature phytase polypeptide for
XX enhancing the phosphorus nutrition of a plant, the growth of a plant on
XX a phosphorus source and the phosphorus content of a plant.
XX Claim 10; Fig 2; 144pp; English.
XX The invention relates to a method of modifying plant productivity
XX which involves expressing phytase (Phy) A gene from Aspergillus niger,
XX in a plant cell. Phytase gene is capable of facilitating plants
XX ability to utilise soil phosphorus. It is used to enhance the
XX phosphorus nutrition of a plant or the growth of a plant on a
XX phosphorus source comprising phytate and/or increase the
XX phosphorus content of a plant. This gene is used to enhance
XX the biomass produced by a plant and also to enhance the rate
XX of hypocotyl production or the rate of epicotyl production.
XX Transgenic plant containing phytase gene has improved productivity
XX than its isogenic counterparts.
XX The present sequence is carrot extensin leader peptide-A. niger
XX phytase A-1 chimeric protein. This chimeric protein is used to
XX enhance phosphorus nutrition in plants.
XX Sequence 482 AA;
XX Query Match 100.0%; Score 2334; DB 22; Length 482;
XX Best Local Similarity 100.0%; Pred. No. 2.7e-214;

Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASRNQSSCCTVDOGYCCFSETSHLWGOVAPFFSLANESVISEVPAGCRVTFAQVLSRHG 60
 DB 39 ASRNQSSCCTVDOGYCCFSETSHLWGOVAPFFSLANESVISEVPAGCRVTFAQVLSRHG 98
 QY 61 ARYPDTSKGGKYSALIEEIQONATTFDQKYAPLKTNYNSLQADDLTPFGEQELVNSGKIF 120
 DB 99 ARYPDTSKGGKYSALIEEIQONATTFDQKYAPLKTNYNSLQADDLTPFGEQELVNSGKIF 158
 QY 121 YORYESLTRNIVFFIRSSGSRVIAAGKFFEGQSTKLKQRAQPGSSPKIDVYSEA 180
 DB 159 YORYESLTRNIVFFIRSSGSRVIAAGKFFEGQSTKLKQRAQPGSSPKIDVYSEA 218
 QY 181 SSSNNTLDPGCTCTVFEDSELADTVEANFTATVPSSIRORLENDLSGVTLTDTEVTYLYDM 240
 DB 219 SSSNNTLDPGCTCTVFEDSELADTVEANFTATVPSSIRORLENDLSGVTLTDTEVTYLYDM 278
 QY 241 CSFDTISTSTVDTKLSPFCDLTHDEWINYDLSLKKYKYGAGNPLGPTQGVGYANEL 300
 DB 279 CSFDTISTSTVDTKLSPFCDLTHDEWINYDLSLKKYKYGAGNPLGPTQGVGYANEL 338
 QY 301 IARLTHSPVHDDTSSNHTLDSGSPATFPKNTSLYADFSDHNGIISILFALGLVNGTKPLST 360
 DB 339 IARLTHSPVHDDTSSNHTLDSGSPATFPKNTSLYADFSDHNGIISILFALGLVNGTKPLST 398
 QY 361 TTVENITQDGFSSAWTVFPASRLYVEMMQCAEQEPLVRLVNDRVVPLHGPCVDALGR 420
 DB 399 TTVENITQDGFSSAWTVFPASRLYVEMMQCAEQEPLVRLVNDRVVPLHGPCVDALGR 458
 QY 421 CTRDSFVRLGSLFARSGGDWAECEFA 444
 DB 459 CTRDSFVRLGSLFARSGGDWAECEFA 482

RESULT 8

AAR4362
 ID AAR4360 standard; Protein: 467 AA.
 AC AAR4360;
 XX
 DT 25-MAR-2003 (updated)
 DT 09-DEC-1991 (first entry)
 XX
 DE Phytase.
 XX
 KW Transgenic plants; inositol.
 XX
 OS Aspergillus ficuum strain NRRJ 3135.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..23
 FT /note= "signal peptide"
 FT Peptide 24..444
 FT /note= "mature peptide"
 XX
 EP449375-A.
 FN
 XX
 PC 02-OCT-1991.
 XX
 PF 25-MAR-1991; 91EP-0200687.
 XX
 PR 21-SEP-1990; 90US-0586765.
 PR 23-MAR-1990; 90US-0498561.
 XX
 XX (KONN) GIST-BROCADES NV.
 PA (MOGE-) MOGEN INT NV.
 PA (STAM) DSM NV.
 XX
 XX Pen J, Hoekema A, Sijmons PC, Vanocoyen Acc, Rietveld K;
 PI Verwoerd TC;
 XX WPI: 1991-289814/40.
 DR

DR N-PSDB; AAQ13878.
 XX
 PT Phytase prodn. transgenic plants or plant organs - used in e.g.
 PT foods or feedstuffs for prodn. of inositol and inorganic
 PT phosphate from phytate.
 XX
 PS Disclosure; Fig 2; 28pp; English.
 XX
 CC The amino acid sequence codes for phytase which catalyses the
 CC conversion of phytate to inositol and inorganic phosphorus. The
 CC phytase given here, obtd. from Aspergillus ficuum, has been
 CC determined to possess one of the highest levels of specific
 CC activity as well as having better thermostability than phytases
 CC produced by other microorganisms. It can also be used as a feed
 CC additive for non-ruminants to promote growth and also to reduce
 CC the phosphorus content of animal manure. It may also be used in
 CC e.g. soy processing, in the starch and fermentation industries and
 CC in steeping of corn or sorghum kernels. See also EP-449375.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 467 AA;
 Query Match 99.5%; Score 2122; DB 12; Length 467;
 Best Local Similarity 99.5%; Pied. No. 3.7e-213;
 Matches 442; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASRNQSSCCTVDOGYCCFSETSHLWGOVAPFFSLANESVISEVPAGCRVTFAQVLSRHG 60
 DB 24 ASRNQSSCCTVDOGYCCFSETSHLWGOVAPFFSLANESVISEVPAGCRVTFAQVLSRHG 83
 QY 61 ARYPDTSKGGKYSALIEEIQONATTFDQKYAPLKTNYNSLQADDLTPFGEQELVNSGKIF 120
 DB 94 ARYPDTSKGGKYSALIEEIQONATTFDQKYAPLKTNYNSLQADDLTPFGEQELVNSGKIF 143
 QY 121 YORYESLTRNIVFFIRSSGSRVIAAGKFFEGQSTKLKQRAQPGSSPKIDVYSEA 180
 DB 144 YORYESLTRNIVFFIRSSGSRVIAAGKFFEGQSTKLKQRAQPGSSPKIDVYSEA 203
 QY 181 SSSNNTLDPGCTCTVFEDSELADTVEANFTATVPSSIRORLENDLSGVTLTDTEVTYLYDM 240
 DB 204 SSSNNTLDPGCTCTVFEDSELADTVEANFTATVPSSIRORLENDLSGVTLTDTEVTYLYDM 263
 QY 241 CSFDTISTSTVDTKLSPFCDLTHDEWINYDLSLKKYKYGAGNPLGPTQGVGYANEL 300
 DB 264 CSFDTISTSTVDTKLSPFCDLTHDEWINYDLSLKKYKYGAGNPLGPTQGVGYANEL 323
 QY 301 IARLTHSPVHDDTSSNHTLDSGSPATFPKNTSLYADFSDHNGIISILFALGLVNGTKPLST 360
 DB 324 IARLTHSPVHDDTSSNHTLDSGSPATFPKNTSLYADFSDHNGIISILFALGLVNGTKPLST 383
 QY 361 TTVENITQDGFSSAWTVFPASRLYVEMMQCAEQEPLVRLVNDRVVPLHGPCVDALGR 420
 DB 384 TTVENITQDGFSSAWTVFPASRLYVEMMQCAEQEPLVRLVNDRVVPLHGPCVDALGR 443
 QY 421 CTRDSFVRLGSLFARSGGDWAECEFA 444
 DB 444 CTRDSFVRLGSLFARSGGDWAECEFA 467

RESULT 9

AAB20505
 ID AAB20505 standard; Protein: 441 AA.
 AC AAB20505;
 XX
 DT 05-DEC-2000 (first entry).
 XX
 DE Aspergillus niger NRRJ3135 phytase SEQ ID NO:5.
 XX
 KW Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
 KW temperature stability; pH profile; temperature profile; reaction rate;
 KW specific activity; substrate specificity; substrate cleavage pattern;

KW substrate binding; position specificity; phytate degradation rate;
 KW food; feed; phytate; manure.
 XX Aspergillus niger.
 XX WO200043503-A1.
 XX PN
 XX PD 27-JUL-2000.
 XX PF 21-JAN-2000; 2000WO-DK00025.
 XX PR 22-JAN-1999; 99DK-0000092.
 XX PR 21-SEP-1999; 99DK-0001340.
 XX FA (NOVC) NOVO NORDISK AS.
 XX PI Lehmann M;
 XX DR WPI; 2000-49:161/43.
 XX XX Novel phytases with improved properties such as temperature stability,
 PT pH stability and substrate specificity, for use in pharmaceuticals and
 PT compound foods and feeds -
 XX PS
 XX PS Example 1; Fig 1a-d; 240pp; English.
 XX CC The present invention describes improved phytases, preferably with
 CC increased thermostability, and methods for producing them. The methods
 CC can be used for producing phytases with improved properties e.g.
 CC temperature stability, pH stability, pH profile, temperature profile,
 CC specific activity, substrate specificity, substrate cleavage pattern,
 CC substrate binding, position specificity, the velocity and level of
 CC release of phosphate from corn, reaction rate, phytate degradation rate,
 CC and end level of released phosphate. The phytases can be used to produce
 CC pharmaceutical compositions or compound food or feeds. The feed can be
 CC used to reduce levels of phytate in animal manure, by converting it
 CC into lower inositol phosphates and/or inositol and inorganic phosphate.
 CC The present sequence represents a phytase sequence from the present
 CC invention.
 XX XX
 XX SQ

QY	4	NQSSCTVDCGYQCFSTSLWGOYAPFFSLANESVISPVPAGCRVTFPAQLSRGARY	63
DB	1	NQSSCTVDCGYQCFSTSLWGOYAPFFSLANESVISPVPAGCRVTFPAQLSRGARY	60
QY	64	PTDSKGGKYSAITFEIQNATTFDCKYAFILKTYNSLGGADLTFPGSEQLNNGIKFYQR	123
DB	61	PTDSKGGKYSAITFEIQNATTFDCKYAFILKTYNSLGGADLTFPGSEQLNNGIKFYQR	120
QY	124	YESLTRNIVPFRSSGSRVIASSKKFIEGQSTKCEPRAQCGQSPKIDWISBASSS	183
DB	121	YESLTRNIVPFRSSGSRVIASSKKFIEGQSTKCEPRAQCGQSPKIDWISBASSS	180
QY	184	NNTLPDGTCTVFDESELAQTVANFTATFVPSIRQRLENLSGVTLTDTETVTLXMCMSF	243
DB	181	NNTLPDGTCTVFDESELAQTVANFTATFVPSIRQRLENLSGVTLTDTETVTLXMCMSF	240
QY	244	DTISTSTVCTKLSPFCDLFTHEMINVDYJOSLKKYVGHGAGNPLGTCQGVGANELIAR	303
DB	241	DTISTSTVCTKLSPFCDLFTHEMINVDYJOSLKKYVGHGAGNPLGTCQGVGANELIAR	300
QY	304	LTHSPVHDDTSSNHTLDSSPATFPNSTLYADFSDHNGIISILFALGLYNGEKLSTTV	363
DB	301	LTHSPVHDDTSSNHTLDSSPATFPNSTLYADFSDHNGIISILFALGLYNGEKLSTTV	360
QY	364	ENITQTGDFSSAWTPVFASRLYVEMMOCAQOEPLVRLVNDRVVPLHGGCFVDALGCTR	423
DB	361	ENITQTGDFSSAWTPVFASRLYVEMMOCAQOEPLVRLVNDRVVPLHGGCFVDALGCTR	420

Query Match	99.4%	Score 2321	DB 21	Length 441
Best Local Similarity	100.0%	Pred. No. 4.2e-213		
Matches 441	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	4	NOSSCDTVDOGQCCESETSHLWGVAPFFS;ANESV;SPWEAGCRVTFQAQLNSRGASY	63
DB	1	NOSSCDTVDOGQCCESETSHLWGVAPFFS;ANESV;SPWEAGCRVTFQAQLNSRGASY	60
QY	64	PTDSKGKKYSALIEIQONATTFQCKYAFLLKTYNYSAGADLLTFEGQELWNSGIFYOR	123
DB	61	PTDSKGKKYSALIEIQONATTFQCKYAFLLKTYNYSAGADLLTFEGQELWNSGIFYOR	120
QY	124	YSLSRNIVPFRSSGSRVSIASGKKFEGFQSTKLKDPFAQPCQSSPKIDVW;SEASSS	183
DB	121	YSLSRNIVPFRSSGSRVSIASGKKFEGFQSTKLKDPFAQPCQSSPKIDVW;SEASSS	180
QY	184	NNTLDPGTCVTFDSDELACTVEANFTAFVPSIRQRLENCLSGVLTPTDTEVTVLMCMCSF	243
DB	181	NNTLDPGTCVTFDSDELACTVEANFTAFVPSIRQRLENCLSGVLTPTDTEVTVLMCMCSF	240
QY	244	DTLSTSTVTKLSPFCDLPTHDEWNIYDY;LSLKKYXGHGAGNPLGTCQGVYANELIAR	303
DB	241	DTLSTSTVTKLSPFCDLPTHDEWNIYDY;LSLKKYXGHGAGNPLGTCQGVYANELIAR	300
QY	304	LTHSPVHDDTSSNHTLDSSPAFTF;NSTLYADFSHNGIITSILFALGLYNGTKPLSTTTV	363
DB	301	LTHSPVHDDTSSNHTLDSSPAFTPLNSLYADFSHNGIITSILFALGLYNGTKPLSTTTV	360
QY	364	ENITQTDGESSAWTVFASRLYVEMMQCAOSEPLVRLVNDVRVVPJHGCFVDALGRCTR	423
DB	361	ENITQTDGESSAWTVFASRLYVEMMQCAOSEPLVRLVNDVRVVPJHGCFVDALGRCTR	420

QY 424 DSFVRGLSFARSGGDWAECPA 444
 DB 421 DSFVRGLSFARSGGDWAECPA 441
 RESULT 10
 AAY69548
 ID AAY69548 standard; protein; 441 AA.
 XX AC AAY69548;
 XX DT 19-APR-2000 (first entry)
 XX DE Aspergillus niger strain NRRL3135 mature phytase.
 XX KW Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation;
 KW thermostable; animal feed; monogastric animal; phytate phosphorus;
 KW phosphate availability.
 XX OS Aspergillus niger str. NRRL3135.
 XX PN EP989083-A1.
 XX PC 05-JAN-2000.
 XX PF 23-JUN-1999; 99EP-0111949.
 XX PR 29-JUN-1998; 98EP-0111960.
 XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX PI Brugger R, Lehmann M, Wyss M;
 XX DR WPI; 2000-099429/09.
 XX PT New stabilized enzyme formulation, useful for feed compositions for
 PT monogastric animals -
 XX PS
 XX PS Example 3; Fig 13; 101pp; English.
 XX CC The invention relates to a novel stabilised dry or liquid enzyme
 CC formulation, comprising phytase (myo-inositol hexakisphosphate
 CC phosphohydrolase) and one or more stabilising agents including
 CC xylitol or ribitol; polyethylene glycols with a molecular weight of 600
 CC to 4000 Da; preferably 1000 to 3350 Da; the disodium salts of malonic,
 CC glutaric and succinic acid; carboxymethyl-cellulose; and sodium alginate.
 CC The stabilised phytase formulation is used in a method for preparing a
 CC feed composition for monogastric animals (e.g., pigs, poultry) and
 CC provides a monogastric animal with its dietary requirements of
 CC phosphorus. Although a large amount of phosphate is present in animal
 CC feed in the form of phytate phosphorus, monogastric animals are unable
 CC to utilise this form of phosphate, resulting in the addition of extra
 CC phosphate to the feed of such animals. Phytase enhances the nutritional
 CC value of plant material without the need for adding additional phosphate
 CC to the feed. The level of phosphate pollution in the environment is
 CC reduced by adding phytase to animal feed, as the animal can make use of
 CC the inorganic phosphate liberated from phytate phosphorus using the
 CC enzyme. The phytase formulation of the invention has an improved
 CC thermostability and can therefore remain stable during long-term storage
 CC and can withstand feed processing methods such as extrusion, expansion
 CC and pelleting. Sequences AAY69544-Y69556 represent the amino acid
 CC sequences of mature phytases from a variety of fungi (mainly different
 CC strains of Aspergillus species), which were used in an exemplification of
 CC the present invention to determine a consensus phytase sequence.
 CC designated phytase-1 (AAY69558). An initial consensus sequence, AAY69557,
 CC was determined using the program PRETTY, and the phytase-1 consensus
 CC derived from the initial consensus. Consensus phytase sequences were
 CC produced in the exemplifications, as a prior art consensus phytase
 CC sequence was found to have higher thermal stability than native
 XX phytases.
 XX SQ Sequence 441 AA;

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Query Match      99.4%; Score 2321; DB 21; Length 441;
Best Local Similarity 100.0%; Pred. No. 4.2e-213;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cc 4 NOSSCDTVDGQYCFSETSHLWGYAFPFSLANESVISPVEVAGCRVTFQAQVLSRHGARY 63
Cc 1 NOSSCDTVDGQYCFSETSHLWGYAFPFSLANESVISPVEVAGCRVTFQAQVLSRHGARY 60
Cc 64 PTDSKGGKYSALIEEIQONATTFDGKYAFKTYNYSLGADLTFFGQELVNSGKIFYOR 123
Cc 61 PTDSKGGKYSALIEEIQONATTFDGKYAFKTYNYSLGADLTFFGQELVNSGKIFYOR 120
Cc 124 YESLTRNIVPFRSSGSRVSIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDWISASSS 183
Cc 121 YESLTRNIVPFRSSGSRVSIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDWISASSS 180
Cc 184 NNTLDPGTCTVFEDSELADTVEANFTATFVPSIRORLENDLSGVLTDTDEVYVMDMCSF 243
Cc 181 NNTLDPGTCTVFEDSELADTVEANFTATFVPSIRORLENDLSGVLTDTDEVYVMDMCSF 240
Cc 244 DTISTSTVDTKLSPPCDLFTHDEWNYDYQSLKYYGHHGAGNPLGPTQGVGVANELIAR 303
Cc 241 DTISTSTVDTKLSPPCDLFTHDEWNYDYQSLKYYGHHGAGNPLGPTQGVGVANELIAR 300
Cc 304 LTHSPVHDDTSSNHTLDSSPA:FPPLNSTLYADFSHONGIISILFALGLYNGTKPJSTTV 363
Cc 301 LTHSPVHDDTSSNHTLDSSPA:FPPLNSTLYADFSHONGIISILFALGLYNGTKPJSTTV 360
Cc 364 ENITQTDGFSSAWTVFASRLVYVEMMQCAOEPLVRV:VNDRVVPLHGPCVDALGRCTR 423
Cc 361 ENITQTDGFSSAWTVFASRLVYVEMMQCAOEPLVRV:VNDRVVPLHGPCVDALGRCTR 420
Cc 424 DSFVRGLSFARSGGDWAECEFA 444
Cc 421 DSFVRGLSFARSGGDWAECEFA 441

Query Match      99.4%; Score 2291; DB 21; Length 441;
Best Local Similarity 98.0%; Pred. No. 3.1e-210;
Matches 432; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Cc 4 NOSSCDTVDGQYCFSETSHLWGYAFPFSLANESVISPVEVAGCRVTFQAQVLSRHGARY 63
Cc 1 NOSSCDTVDGQYCFSETSHLWGYAFPFSLANESVISPVEVAGCRVTFQAQVLSRHGARY 60
Cc 64 PTDSKGGKYSALIEEIQONATTFDGKYAFKTYNYSLGADLTFFGQELVNSGKIFYOR 123
Cc 61 PTDSKGGKYSALIEEIQONATTFDGKYAFKTYNYSLGADLTFFGQELVNSGKIFYOR 120
Cc 124 YESLTRNIVPFRSSGSRVSIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDWISASSS 183
Cc 121 YESLTRNIVPFRSSGSRVSIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDWISASSS 180
Cc 184 NNTLDPGTCTVFEDSELADTVEANFTATFVPSIRORLENDLSGVLTDTDEVYVMDMCSF 243
Cc 181 NNTLDPGTCTVFEDSELADTVEANFTATFVPSIRORLENDLSGVLTDTDEVYVMDMCSF 240
Cc 244 DTISTSTVDTKLSPPCDLFTHDEWNYDYQSLKYYGHHGAGNPLGPTQGVGVANELIAR 303
Cc 241 DTISTSTVDTKLSPPCDLFTHDEWNYDYQSLKYYGHHGAGNPLGPTQGVGVANELIAR 300
Cc 304 LTHSPVHDDTSSNHTLDSSPA:FPPLNSTLYADFSHONGIISILFALGLYNGTKPJSTTV 363
Cc 301 LTHSPVHDDTSSNHTLDSSPA:FPPLNSTLYADFSHONGIISILFALGLYNGTKPJSTTV 360
Cc 364 ENITQTDGFSSAWTVFASRLVYVEMMQCAOEPLVRV:VNDRVVPLHGPCVDALGRCTR 423
Cc 361 ENITQTDGFSSAWTVFASRLVYVEMMQCAOEPLVRV:VNDRVVPLHGPCVDALGRCTR 420
Cc 424 DSFVRGLSFARSGGDWAECEFA 444
Cc 421 DSFVRGLSFARSGGDWAECEFA 441

RESULT 12
AAR46792
ID AAR46792 standard; protein; 441 AA.
AC AAY69547;
CZ 19-APR-2000 (first entry)
DE Aspergillus niger T213 mature phytase.
KW Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation;
KW thermostable; animal feed; monogastric animal; phytate phosphorus;
KW phosphate availability.
XX
XX Aspergillus niger T213.
XX OS
XX PN
XX EP969089-A1.
XX PD
XX 05-JAN-2000.
XX PF
XX 23-JUN-1999; 98EP-0111949.
XX PR
XX 29-JUN-1998; 98EP-0111960.
XX PA
XX (HOPF ) HOFFMANN LA ROCHE & CO AG F.
XX PI
XX Brugger R, Lehmann M, Wyss M;
XX DR
XX WPI; 2000-099429/09.
XX PT
XX New stabilized enzyme formulation, useful for feed compositions for
XX monogastric animals -
XX Example 3; Fig 13; 101pp; English.
XX PS
XX

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The invention relates to a novel stabilised dry or liquid enzyme formulation, comprising phytase (myo-inositol hexakisphosphate phosphohydrolase) and one or more stabilising agents including xylitol or ribitol; polyethylene glycols with a molecular weight of 600 to 4000 Da, preferably 1000 to 3350 Da; the disodium salts of alonic, glutaric and succinic acid; carboxymethylcellulose; and sodium alginate. The stabilised phytase formulation is used in a method for preparing a feed composition for monogastric animals (e.g., pigs, poultry) and provides a monogastric animal with its dietary requirements of phosphorus. Although a large amount of phosphate is present in animal feed in the form of phytate phosphorus, monogastric animals are unable to utilise this form of phosphate, resulting in the addition of extra phosphate to the feed of such animals. Phytase enhances the nutritional value of plant material without the need for adding additional phosphate to the feed. The level of phosphate pollution in the environment is reduced by adding phytase to animal feed, as the animal can make use of the inorganic phosphate liberated from phytate phosphorus using the enzyme. The phytase formulation of the invention has an improved thermostability and can therefore remain stable during long-term storage and can withstand feed processing methods such as extrusion, expansion and pelleting. Sequences AAY69544-Y69556 represent the amino acid sequences of mature phytases from a variety of fungi (mainly different strains of *Aspergillus* species), which were used in an exemplification of the present invention to determine a consensus phytase sequence, designated phytase-1 (AAY69558). An initial consensus sequence, AAY69557, was determined using the program PRETTY, and the phytase-1 consensus was derived from the initial consensus. Consensus phytase sequences were produced in the exemplifications, as a prior art consensus phytase sequence was found to have higher thermal stability than native phytases.

Sequence 441 AA;

Query Match 98.2%; Score 2291; DB 21; Length 441;
 Best Local Similarity 98.0%; Pred. No. 3.1e-210;
 Matches 432; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

CY 4 NOSSCDTVDGQYCFSETSHLWGYAFPFSLANESVISPVEVAGCRVTFQAQVLSRHGARY 63
 DB 1 NOSSCDTVDGQYCFSETSHLWGYAFPFSLANESVISPVEVAGCRVTFQAQVLSRHGARY 60
 CY 64 PTDSKGGKYSALIEEIQONATTFDGKYAFKTYNYSLGADLTFFGQELVNSGKIFYOR 123
 DB 61 PTDSKGGKYSALIEEIQONATTFDGKYAFKTYNYSLGADLTFFGQELVNSGKIFYOR 120
 CY 124 YESLTRNIVPFRSSGSRVSIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDWISASSS 183
 DB 121 YESLTRNIVPFRSSGSRVSIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDWISASSS 180
 CY 184 NNTLDPGTCTVFEDSELADTVEANFTATFVPSIRORLENDLSGVLTDTDEVYVMDMCSF 243
 DB 181 NNTLDPGTCTVFEDSELADTVEANFTATFVPSIRORLENDLSGVLTDTDEVYVMDMCSF 240
 CY 244 DTISTSTVDTKLSPPCDLFTHDEWNYDYQSLKYYGHHGAGNPLGPTQGVGVANELIAR 303
 DB 241 DTISTSTVDTKLSPPCDLFTHDEWNYDYQSLKYYGHHGAGNPLGPTQGVGVANELIAR 300
 CY 304 LTHSPVHDDTSSNHTLDSSPA:FPPLNSTLYADFSHONGIISILFALGLYNGTKPJSTTV 363
 DB 301 LTHSPVHDDTSSNHTLDSSPA:FPPLNSTLYADFSHONGIISILFALGLYNGTKPJSTTV 360
 CY 364 ENITQTDGFSSAWTVFASRLVYVEMMQCAOEPLVRV:VNDRVVPLHGPCVDALGRCTR 423
 DB 361 ENITQTDGFSSAWTVFASRLVYVEMMQCAOEPLVRV:VNDRVVPLHGPCVDALGRCTR 420
 CY 424 DSFVRGLSFARSGGDWAECEFA 444
 DB 421 DSFVRGLSFARSGGDWAECEFA 441

RESULT 12
 AAR46792
 ID AAR46792 standard; protein; 467 AA.

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XX AC AAR46792;
XX DT 25-MAR-2003 (updated);
XX DT 19-AUG-1994 (first entry);
XX DE Phytase.
XX KW pH 2.5; acid phosphatase; Trichoderma; host; Aspergillus; phytic acid;
XX KW phytate degrading enzyme; PDE; removal; inositol hexaphosphoric acid;
XX KW p-ant; feed composition; filtration.
XX CS Aspergillus niger.
XX FH Key Location/Qualifiers
XX FT Peptide 1..19
XX FT /note= "Signal peptide"
XX FT Protein 20..467
XX FT /note= "Mature phytase"
XX PN W09403612-A1.
XX PC 17-FEB-1994.
XX PF 30-JUL-1993; 93WO-F10310.
XX PR 31-JUL-1992; 92US-0923724.
XX PA (ALCO-) ALKO LTD.
XX PI Cantrell M, Fagerstrom RB, Miettinen-Oinonen ASK;
XX PI Nevalainen HK, Palcheimo MT, Piddington C, Rambosek JA;
XX PI Torkkeli TK, Turunen MK;
XX DR WPI; 1994-065700/08.
XX DR N-PSDB; AAC59126.
XX CS Carpers. contg. phytate degrading enzymes - obtd. by expression
XX PT of their genes in Trichoderma, used partic. for producing animal
XX PT feed compens.
XX PS Claim 3; Fig 5; 142pp; English.
XX CC This sequence represents a phytase which was used in the production of
XX CC the composition of the invention. This sequence may be introduced
XX CC into a Trichoderma host which then expresses it and the protein is
XX CC collected from the culture medium. By using Trichoderma as a host
XX CC for Aspergillus phytate degrading enzymes such as this, a totally
XX CC different enzyme composition compared to that secreted from
XX CC Aspergillus results. The enzyme composition can be used for removal
XX CC of phytic acid or inositol hexaphosphoric acid from raw material,
XX CC particularly plant material. The composition is used in feed
XX CC compositions for animals. By using Trichoderma as a source of a
XX CC composition containing phytate degrading enzymes some difficult
XX CC downstream processing problems, eg. filtration, that occur with
XX CC similar Aspergillus compositions are avoided and yields are improved.
XX CC (Updated on 25-MAR-2003 to correct EN field.)
XX SQ Sequence 467 AA;

Query Match 98.1%; Score 2290; DB 15; Length 467;
Best Local Similarity 97.3%; Pred. No. 4.3e-210;
Matches 432; Conservative 8; Mismatches 4; Indels C; Gaps 0;

QY 1 ASRNQSCDTVDQYQCFSETSHLWGQYAPFSSLANESVTSPEVPACRVTFAQVLSRHG 60
DB [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]
24 ASRNQSCDTVDQYQCFSETSHLWGQYAPFSSLANESVTSPEVPACRVTFAQVLSRHG 83
QY 61 ARYETDSKGYKYSALIEICQNAITFGKYAFILKTYNYS;GADDLTPFGQELVNSGIKF 120
DB [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]
84 ARYETDSKGYKYSALIEICQNAITFGKYAFILKTYNYS;GADDLTPFGQELVNSGIKF 143
QY 121 YORVESLTRNIVPIRSSGSSRVIASGKFTEGQSTKLKDPRAQPGSSPKIDWISEA 190
DB [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]
144 YORVESLTRNIVPIRSSGSSRVIASGKFTEGQSTKLKDPRAQPGSSPKIDWISEA 203
QY [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]
191 SSSNNLTDPGTCVTFEDELADTVEANFTATFVPSIFQRLENDLSGVTLTDTETVYLMDM 240
DB [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]
204 SSSNNLTDPGTCVTFEDELADTVEANFTATFASIRQRLENDLSGVTLTDTETVYLMDM 263
QY [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]
241 CSFDTISTSTVDTKLSPPCDLFTHDEWINKYDLSLKKYGGAGNPLGPTQGVYANEL 300
DB [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]
264 CSFDTISTSTVDTKLSPPCDLFTHDEWINKYDLSLKKYGGAGNPLGPTQGVYANEL 323
QY [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]
301 IARLTHSPVHDTSSNHTLDSRPATEPLNSTCYADFSDHNGIISILFALGLYNGTKELST 360
DB [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]
324 IARLTHSPVHDTSSNHTLDSRPATEPLNSTCYADFSDHNGIISILFALGLYNGTKELST 383
QY [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]
361 TTVENITQDGFSSANTVPPFASRLYVEMMQCAEPLRVLYLVNDRVVPVFLHGCPIDALGR 420
DB [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]
384 TTVENITQDGFSSANTVPPFASRLYVEMMQCAEPLRVLYLVNDRVVPVFLHGCPIDALGR 443
QY [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]
421 CTRDSFVRGLSPARSGGDAECFA 444
DB [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]
444 CTRDSFVRGLSPARSGGDAECFA 467

RESULT 13
AAR46234 standard; Protein; 467 AA.
XX AC AAR46234;
XX DT 25-MAR-2003 (updated)
XX DT 01-SEP-1994 (first entry);
XX DE A. niger phytase.
XX KW Phytase; pH 2.5 acid phosphatase; A. niger; strain ALK0243; mineral;
XX KW liberation; phytate; plant material; feed treatment; animal; inositol;
XX KW enzyme mixture; hydrolysis; phosphate; phytic acid complex.
XX CS Aspergillus niger var. awamori; strain ALK0243.
XX FH Key Location/Qualifiers
XX FT Peptide 407..422
XX FT /note= "Peptide #420"
XX PN W09403572-A1.
XX PC 17-FEB-1994.
XX PF 27-JUL-1993; 93WO-US07059.
XX PR 31-JUL-1992; 92US-0925401.
XX PA (ALCO-) ALKO LTD.
XX PA (NEVA/) NEVALAINEN H K M.
XX PA (PANL-) PANLABS INC.
XX PI Cantrell MA, Fagerstrom RB, Houston CS, Miettinen-Oinonen ASK;
XX PI Palcheimo MT, Piddington CS, Rambosek JA, Turunen MK;
XX DR WPI; 1994-065302/C8.
XX DR N-PSDB; AAC56944.
XX PT Nucleic acid encoding phytase and pH 2.5 acid phosphatase - used
XX PT to produce the enzymes and enzyme mixts. for liberating minerals
XX PT from phytate, partic. for animal feed
XX PS Claim 1; Fig 9; 103pp; English.
XX CC The sequences given in AAR46234-35 represent the phytase and pH 2.5 acid
XX CC phosphatase from A. niger var. awamori strain ALK0243. The cDNA
XX CC encoding these sequences was used to transform host cells for the
XX CC expression of the phytase and phosphatase. The phytase and pH 2.5 acid

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CC phosphatase proteins can be used to liberate minerals from phytates
 CC in plant materials either in vitro, ie, in feed treatment processes,
 CC or in vivo, ie, by administering the enzymes to animals. The
 CC enzymes can be mixed to provide a balanced enzyme mixture in which
 CC cooperative enzyme activity rapidly and effectively catalyses the
 CC near complete hydrolysis of phytate to inositol and free phosphate
 CC with release of minerals from the phytic acid complex.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 467 AA;

Query Match 98.1%; Score 2290; DB 15; Length 467;
 Best Local Similarity 97.3%; Pred. No. 4.3e-210;
 Matches 432; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
 QY 1 ASRQSSCDTVDQGYQCFSETHLWGQVAPFFSLANESVISPAGCRVTFACVLSRHG 60
 DB 24 ASRQSSCDTVDQGYQCFSETHLWGQVAPFFSLANESA-SPDVPAGCRVTFACVLSRHG 83
 QY 61 ARYPTSGKKYSALIEIEIQONATTFDQKYAFPLKTYNYSLGADDLTPFGCELVNSGKFP 120
 DB 84 ARYPTSGKKYSALIEIEIQONATTFDQKYAFPLKTYNYSLGADDLTPFGCELVNSGKIF 143
 QY 121 YQVESLNRNVPFRIRSSGSRVVASGKFEFGQSTKLKDPFRAQPGSSPKIDVWISA 180
 DB 144 YQVESLNRNVPFRIRSSGSRVVASGKFEFGQSTKLKDPFRAQPGSSPKIDVWISA 203
 QY 181 SSSNNTLDPGCTVFEDSELADTVEANFTATFVPSIRQRLNDSLVTLTDTETVYLMQV 240
 DB 204 SSSNNTLDPGCTVFEDSELADTVEANFTATFAPSIRQRLNDSLVTLTDTETVYLMQV 263
 QY 241 CSFTTISTVDTKLSFPCDLFTHDEWINDYLSLKKYVGHGAGNPLGPTQGVYANEL 300
 DB 264 CSFTTISTVDTKLSFPCDLFTHDEWINDYLSLKKYVGHGAGNPLGPTQGVYANEL 323
 QY 361 IARLTHSPVHDTSSNHTLDSSPATFPKNSLYADFSDHNGIISILFALGLYNGTKPST 360
 DB 324 IARLTHSPVHDTSSNHTLDSSPATFPKNSLYADFSDHNGIISILFALGLYNGTKPST 383
 QY 361 TTVENITQDGFSSAWTVFFASRLYVENMQCAEQEPLVRVLRVDRVVPVPHGCPVDALGR 420
 DB 384 TTVENITQDGFSSAWTVFFASRLYVENMQCAEQEPLVRVLRVDRVVPVPHGCPVDALGR 443
 QY 421 CTRDSFVRLGSLFARSGGDAECFA 444
 DB 444 CTRDSFVRLGSLFARSGGDAECFA 467

RESULT 14
 AAB20504
 ID AAB20504 standard; Protein: 441 AA.

XX AC AAB20504;

DT 05-DEC-2000 (first entry)

DE Aspergillus niger T23 phytase SEQ ID NO:4.

XX Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
 KW temperature stability; pH profile; temperature profile; reaction rate;
 KW specific activity; substrate specificity; substrate cleavage pattern;
 KW substrate binding; position specificity; phytate degradation rate;
 KW food; feed; phytate; manure.

XX Aspergillus niger.

XX W0200043503-A1.

XX 27-JUL-2000.

PF 21-JAN-2000; 2000WC-DK00025.

XX 22-JAN-1999; 59DK-0000092.

FR 21-SEP-1999; 95DK-0001340.

XX (NOVO) NOVO NORDISK AS.

XX Lehmann M;

XX WPI; 2000-491161/43.

PT Novel phytases with improved properties such as temperature stability,
 PT pH stability and substrate specificity, for use in pharmaceuticals and
 PT compound foods and feeds -

PS Example 1; Fig 1a-d; 240pp; English.

XX The present invention describes improved phytases, preferably with
 CC increased thermostability, and methods for producing them. The methods
 CC can be used for producing phytases with improved properties e.g.
 CC temperature stability, pH stability, pH profile, temperature profile,
 CC specific activity, substrate specificity, substrate cleavage pattern,
 CC substrate binding, position specificity, the velocity and level of
 CC release of phosphate from corn, reaction rate, phytate degradation rate,
 CC and end level of released phosphate. The phytases can be used to produce
 CC pharmaceutical compositions or compound food or feeds. The feed can be
 CC used to reduce levels of phytate in animal manure, by converting it
 CC into lower inositol phosphates and/or inositol and inorganic phosphate.
 CC The present sequence represents a phytase sequence from the present
 CC invention.

SQ Sequence 441 AA;

Query Match 98.0%; Score 2288; DB 21; Length 441;
 Best Local Similarity 97.7%; Pred. No. 6e-210;
 Matches 431; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

QY 4 NQSSCDTVDQGYQCFSETHLWGQVAPFFSLANESVISPAGCRVTFACVLSRHGARY 63
 DB 1 NQSSCDTVDQGYQCFSETHLWGQVAPFFSLANESVISPAGCRVTFACVLSRHGARY 60
 QY 64 PTDSKGYKYSALIEIEIQONATTFDQKYAFPLKTYNYSLGADDLTPFGCELVNSG-KFYOR 123
 DB 61 PTDSKGYKYSALIEIEIQONATTFDQKYAFPLKTYNYSLGADDLTPFGCELVNSG-KFYOR 120
 QY 124 YESLNRNVPFRIRSSGSRVVASGKFEFGQSTKLKDPFRAQPGSSPKIDVWISA 183
 DB 121 YESLNRNVPFRIRSSGSRVVASGKFEFGQSTKLKDPFRAQPGSSPKIDVWISA 180
 QY 184 NNTLDPGCTVFEDSELADTVEANFTATFVPSIRQRLNDSLVTLTDTETVYLMQV 243
 DB 181 NNTLDPGCTVFEDSELADTVEANFTATFAPSIRQRLNDSLVTLTDTETVYLMQV 240
 QY 244 DTISTVDTKLSFPCDLFTHDEWINDYLSLKKYVGHGAGNPLGPTQGVYANELIAR 303
 DB 241 DTISTVDTKLSFPCDLFTHDEWINDYLSLKKYVGHGAGNPLGPTQGVYANELIAR 300
 QY 304 LTHSPVHDTSSNHTLDSSPATFPKNSLYADFSDHNGIISILFALGLYNGTKPSTTTV 363
 DB 301 LTHSPVHDTSSNHTLDSSPATFPKNSLYADFSDHNGIISILFALGLYNGTKPSTTTV 360
 QY 364 ENITQDGFSSAWTVFFASRLYVENMQCAEQEPLVRVLRVDRVVPVPHGCPVDALGRCTR 423
 DB 361 ENITQDGFSSAWTVFFASRLYVENMQCAEQEPLVRVLRVDRVVPVPHGCPVDALGRCTR 420
 QY 424 DSFVRLGSLFARSGGDAECFA 444
 DB 421 DSFVRLGSLFARSGGDAECFA 441

RESULT 15

AAB20503

ID AAB20503 standard; Protein: 441 AA.

XX AC AAB20503;

```

05-DEC-2000 (first entry)
XX Aspergillus niger var. awamori phytase SEQ ID NO:3.
DE
XX
KW Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
KW temperature stability; pH profile; temperature profile; reaction rate;
KW specific activity; substrate specificity; substrate cleavage pattern;
KW substrate binding; position specificity; phytate degradation rate;
KW food; feed; phytate; manure.
XX
OS Aspergillus niger var. awamori.
XX
PN WO200043503-A1.
XX
PD 27-JUL-2000.
XX
PF 21-JAN-2000; 2000WO-DK0025.
XX
PR 22-JAN-1999; 99DK-000092.
XX
PR 21-SEP-1999; 99DK-0001340.
XX
PA (NOVC ) NOVO MORDISK AS.
XX
PI Lehmann M;
XX
PI WPI; 2000-49116-/43.
XX
PR Novel phytases with improved properties such as temperature stability,
XX pH stability and substrate specificity, for use in pharmaceuticals and
XX compound foods and feeds .
XX
PS Example 1; Fig 1a-d; 240pp; English.
XX
CC The present invention describes improved phytases, preferably with
CC increased thermostability, and methods for producing them. The methods
CC can be used for producing phytases with improved properties e.g.
CC temperature stability, pH stability, pH profile, temperature profile,
CC specific activity, substrate specificity, substrate cleavage pattern,
CC substrate binding, position specificity, the velocity and level of
CC release of phosphate from corn, reaction rate, phytate degradation rate,
CC and end level of released phosphate. The phytases can be used to produce
CC pharmaceutical compositions or compound food or feeds. The feed can be
CC used to reduce levels of phytate in animal manure, by converting it
CC into lower inositol phosphates and/or inositol and inorganic phosphate.
CC The present sequence represents a phytase sequence from the present
CC invention.
XX
SC Sequence 441 AA;

```

```

Query Match 97.6%; Score 2277; DB 21; Length 441;
Best Local Similarity 97.3%; Pred. No. 6, 8e-209;
Matches 429; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 364 LTHSPVHDD:SSNHTLSSSPATFPJNSTLYADPSHENGIIISILFALGLYNGTKPLSTTTV 363
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 361 LTHSPVHDD:SSNHTLSSNPTFPJNSTLYADPSHENGIIISILFALGLYNGTKPLSTTTV 360
QY 364 ENITOTDGFSSAWTVPFASRLVYVEMMOQAQOEPPVRLVNDNRVVPLEGCPVDALGRCTR 423
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 361 ENITOTDGFSSAWTVPFASRLVYVEMMOQAQOEPPVRLVNDNRVVPLEGCPVDALGRCTR 420
QY 424 DSFVRGLSFARSGGWAECFA 444
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 421 DSFVRGLSFARSGGWAECFA 441

```

Search completed: November 12, 2003, 14:31:26
Job time : 48 secs

GenCore version: 5.1.6
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OK protein - protein search, using sw model

Run on: November 12, 2003, 14:29:20 ; Search time 19 Seconds
(without alignments)
2937.830 Million cell updates/sec

Title: US-10-062-848-1

Perfect score: 2334
Sequence: 1 ASRNSQSDTVQGVQCFSE.....SFVRLGFARSGGDWASCEFA 444

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRMSL_23:

- 1: sp.archaea.*
- 2: sp.bacteria.*
- 3: sp.fungi.*
- 4: sp.human.*
- 5: sp.invertebrate.*
- 6: sp.mammal.*
- 7: sp.mhc.*
- 8: sp.organelle.*
- 9: sp.phage.*
- 10: sp.plant.*
- 11: sp.ren.*
- 12: sp.virus.*
- 13: sp.vvertebrate.*
- 14: sp.unclassified.*
- 15: sp.virus.*
- 16: sp.bacteria.*
- 17: sp.archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	2294	98.3	467	Q9UJZ7	Q9UJZ7 aspergillus
2	2260	96.8	48	Q8Z255	Q8Z255 aspergillus
3	2259	96.8	467	Q9JH38	Q9JH38 aspergillus
4	2249	95.4	467	Q9HEQ3	Q9HEQ3 aspergillus
5	1610	69.0	456	Q9C1T1	Q9C1T1 aspergillus
6	1606.5	68.8	463	Q9C092	Q9C092 aspergillus
7	1605.5	68.8	442	Q8KZ75	Q8KZ75 aspergillus
8	1520	65.1	466	Q9C0T0	Q9C0T0 aspergillus
9	1496.5	64.1	466	Q9C096	Q9C096 aspergillus
10	1493	64.0	466	Q9C085	Q9C085 aspergillus
11	1429.5	48.4	487	Q9C107	Q9C107 thelavia h
12	762.5	32.7	443	Q96VF5	Q96VF5 trimeretes pu
13	752.5	32.2	439	Q96VH9	Q96VH9 peniophora
14	739.5	31.7	453	Q96VT0	Q96VT0 agrocycbe pe
15	739	31.7	442	Q96VK9	Q96VK9 cf. ceripor
16	732	31.4	442	Q96VK8	Q96VK8 cf. ceripor

17	357	15.3	482	3	Q9X1W7	Q9X1W7 monascus an
18	355	15.2	469	3	Q9V846	Q9V846 kluyveromyc
19	302.5	13.0	442	3	Q74677	Q74677 pichia angu
20	300	12.9	463	3	C61172	C61172 schizosacch
21	225	9.6	452	1	Q35217	Q35217 rattus norv
22	216	9.3	467	5	Q9VW72	Q9VW72 drosophila
23	212	9.1	431	11	Q8VDR0	Q8VDR0 mus musculu
24	210	9.0	471	11	Q9Z2L6	Q9Z2L6 mus musculu
25	209	9.0	449	13	Q92170	Q92170 gallus gali
26	204	8.7	487	4	Q95172	Q95172 homo sapien
27	203	8.7	487	4	Q9CWX1	Q9CWX1 homo sapien
28	202	8.7	467	5	C95421	C95421 drosophila
29	201	8.6	487	4	Q9JCA3	Q9JCA3 homo sapien
30	185.5	7.9	464	13	Q9CXV1	Q9CXV1 fugu rubrip
31	185	7.9	453	5	Q95420	Q95420 drosophila
32	184	7.9	453	5	Q94438	Q94438 drosophila
33	176.5	7.6	497	10	Q94132	Q94132 arabidopsis
34	157	6.7	274	11	Q9CJDS	Q9CJDS mus musculu
35	148	6.3	210	5	Q8T312	Q8T312 drosophila
36	147	6.3	210	5	Q8T312	Q8T312 drosophila
37	142	6.1	606	16	Q8G772	Q8G772 bifidobacte
38	137.5	5.9	198	3	Q9UTX1	Q9UTX1 schizosacch
39	137.5	5.9	374	11	Q9TMS5	Q9TMS5 mus musculu
40	137.5	5.9	418	11	Q8SP40	Q8SP40 mus musculu
41	136.5	5.8	381	11	Q9QXG5	Q9QXG5 mus musculu
42	132.5	5.7	1341	16	Q8EUS5	Q8EUS5 mycoplasma
43	128	5.5	480	11	Q8Z12	Q8Z12 mus musculu
44	127	5.4	480	11	Q8BHA9	Q8BHA9 mus musculu
45	120.5	5.2	413	16	Q8XB26	Q8XB26 escherichia

ALIGNMENTS

RESULT 1

Q9UJZ7 PRELIMINARY; PRT; 467 AA.
 AC Q9UJZ7
 DT 01-MAY-2000 (TRMSBLrel. 13, Created!
 DT 01-MAY-2000 (TRMSBLrel. 13, Last sequence update;
 DT 01-OCT-2002 (TRMSBLrel. 22, Last annotation update;
 DE Vxo-inositol hexaphosphate phosphohydrolase precursor
 EC 3.1.3.8)
 OS Aspergillus niger.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiaceae; Trichocomaceae; Mitosporic trichocomaceae; Aspergillus.
 CX NCBI_TaxID=5061;
 RN 1.
 PP SEQUENCE FROM N.A.
 PA Hongming W., Qi W., Jing X.;
 RT "PCR cloning and characterization of the phytase (phyA) gene of
 R. Aspergillus niger (China Strain)".
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DP EXBL; AF218813; AAF25461.1;
 DR HSSP; P34752; 11HP.
 DR InterPro; IPR000563; HisAc phsphtse.
 DR Pfam; PF03328; acid phosphat.
 DR PROSITE; PS00616; HIS-ACID-POSPHAT_1; 1.
 DR PROSITE; PS00778; HIS-ACID-POSPHAT_2; 1.
 KW Hydrolyase; Lyase; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 SQ SEQUENCE 467 AA; 51030 MW; F4300A8F165B9F92 CRC64;

Query Match 98.3%; Score 2294; DB 3; Length 467;
 Best Local Similarity 97.5%; Pred. No. 1.9e-167;
 Matches 433; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ASRNSQSDTVQGVQCFSESHLWQVAPFFSLANESVISPEVAGCRVTFQVLSRHG 60

Db 24 ASRNSQSDTVQGVQCFSESHLWQVAPFFSLANESVISPEVAGCRVTFQVLSRHG 83

Cy 61 ARYPTDSKKYSALIEEIQNATTFDGYAFLEKTYNLSLGGADLTTFGEELVNSGKIF 120

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DB 84 ARYPTDSKGGKYSALIEEIQQWATTFDCKYAFELKTYNYSJGADDLTPFGECELVNSGKIF 143
QY 121 YQRYESLTKNIVPFIRSSGSSRVIASGKKF:EGFQSTKLKOPRAQPGQSSPKIDWVISEA 180
DB 144 YQRYESLTKNIVPFIRSSGSSRVIASGKKF:EGFQSTKLKOPRAQPGQSSPKIDWVISEA 203
QY 181 SSSNNTLDPGCTCTVFEDSELADTVANFTATVPFISIRORLND:SGVTLTDTETVYLYMD 240
DB 204 SSSNNTLDPGCTCTVFEDSELADTVANFTATVPFISIRORLND:SGVTLTDTETVYLYMD 263
QY 241 CSFDTISTSTVDTKLSFPCDLTFHDEWKNYDYQSLKKYVGHGAGNPLGPTQGVYANEL 300
DB 264 CSFDTISTSTVDTKLSFPCDLTFHDEWKNYDYQSLKKYVGHGAGNPLGPTQGVYANEL 323
QY 301 IARLTHSPVHDTSSNHTLDSSPA:FPINSLTYADFSDHNGIISILFALGLYNGTKPLST 360
DB 324 IARLTHSPVHDTSSNHTLDSNSATFPINSLTYADFSDHNGIISILFALGLYNGTKPLST 383
QY 361 TTVENITQTDGESSANTVPPFASRLYVEMMQCAEQEPVLRVLVNDRVVPPLHGCVPDALGR 420
DB 384 TTVENITQTDGESSANTVPPFASRLYVEMMQCAEQEPVLRVLVNDRVVPPLHGCVPDALGR 443
QY 421 CTGDSFVRGLSPARSGGDWAECPA 444
DB 444 CTGDSFVRGLSPARSGGDWAECPA 467

RESULT 2
ID Q8J255 PRELIMINARY; PRT: 448 AA.
AC Q8J255;
DT 01-MAR-2003 (Tremblre); 23, Created;
DT 01-MAR-2003 (Tremblre); 23, Last sequence update;
DE PhyCase (Fragment);
GN PHVA.
OS Aspergillus ficuum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes.
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5098;
RN [1]
RP SEQUENCE FROM N.A.
RA Li G., Zhu J., Xu Z., Wang L., Chen G., Jiang H., Li M.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EXBL: AF57344; AAY10115.1;
FT NON-TER
SQ SEQUENCE 448 AA; 49260 MW; 0554FF9712FF7BAA CRC64;

Query Match 96.8%; Score 2260; DB 3; Length 448;
Best Local Similarity 95.5%; Pred. No. 7 4e-165;
Matches 424; Conservative 14; Mismatches 6; Indels 0; Gaps 0;

QY 1 ASRQSCDTPVQGYOCFSETSHLWQYAPFFSLANKSAISPDVAGQVFAQVLSRHG 60
DB 5 ASRQSCDTPVQGYOCFSETSHLWQYAPFFSLANKSAISPDVAGQVFAQVLSRHG 64
QY 61 ARYPTDSKGGKYSALIEEIQQWATTFDCKYAFELKTYNYSJGADDLTPFGECELVNSGKIF 120
DB 65 ARYPTDSKGGKYSALIEEIQQWATTFDCKYAFELKTYNYSJGADDLTPFGECELVNSGKIF 124
QY 121 YQRYESLTKNIVPFIRSSGSSRVIASGKKF:EGFQSTKLKOPRAQPGQSSPKIDWVISEA 180
DB 125 YQRYESLTKNIVPFIRSSGSSRVIASGKKF:EGFQSTKLKOPRAQPGQSSPKIDWVISEA 184
QY 181 SSSNNTLDPGCTCTVFEDSELADTVANFTATVPFISIRORLND:SGVTLTDTETVYLYMD 240
DB 185 STSNNTLDPGCTCTVFEDSELADTVANFTATVPFISIRORLND:SGVTLTDTETVYLYMD 244
QY 241 CSFDTISTSTVDTKLSFPCDLTFHDEWKNYDYQSLKKYVGHGAGNPLGPTQGVYANEL 300
DB 245 CSFDTISTSTVDTKLSFPCDLTFHDEWKNYDYQSLKKYVGHGAGNPLGPTQGVYANEL 304
QY 301 IARLTHSPVHDTSSNHTLDSSPA:FPINSLTYADFSDHNGIISILFALGLYNGTKPLST 360

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DB 305 IARLTHSPVHDTSSNHTLDSSPA:FPINSLTYADFSDHNGIISILFALGLYNGTKPLST 364
QY 361 TTVENITQTDGESSANTVPPFASRLYVEMMQCAEQEPVLRVLVNDRVVPPLHGCVPDALGR 420
DB 365 TTVENITQTDGESSANTVPPFASRLYVEMMQCAEQEPVLRVLVNDRVVPPLHGCVPDALGR 424
QY 421 CTGDSFVRGLSPARSGGDWAECPA 444
DB 425 CTGDSFVRGLSPARSGGDWAECPA 448

RESULT 3
ID C93838 PRELIMINARY; PRT: 467 AA.
AC C93838;
DT 01-MAY-1999 (Tremblre); 10, Created;
DT 01-MAY-1999 (Tremblre); 10, Last sequence update;
DT 01-JUN-2002 (Tremblre); 21, Last annotation update;
DE Phytase.
GN PHVA.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes.
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP SEQUENCE FROM N.A.
RA Nagashima T., Kondo H., Anazawa H., Terasaki Y.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EXBL: AB222700; BAA74433.1;
DR HSP: P34752; IHP.
DR InterPro: IPR003560; HisAc_phosphatase.
DR Pfam: PFO0328; acid_phosphatase; 1.
DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.
SQ SEQUENCE 467 AA; 51028 MW; 7A38ED543EDC265C CRC64;

Query Match 96.8%; Score 2259; DB 3; Length 467;
Best Local Similarity 95.3%; Pred. No. 9 4e-165;
Matches 423; Conservative 14; Mismatches 7; Indels 0; Gaps 0;

QY 1 ASRQSCDTPVQGYOCFSETSHLWQYAPFFSLANKSAISPDVAGQVFAQVLSRHG 60
DB 24 ASRQSCDTPVQGYOCFSETSHLWQYAPFFSLANKSAISPDVAGQVFAQVLSRHG 63
QY 61 ARYPTDSKGGKYSALIEEIQQWATTFDCKYAFELKTYNYSJGADDLTPFGECELVNSGKIF 120
DB 84 ARYPTDSKGGKYSALIEEIQQWATTFDCKYAFELKTYNYSJGADDLTPFGECELVNSGKIF 143
QY 121 YQRYESLTKNIVPFIRSSGSSRVIASGKKF:EGFQSTKLKOPRAQPGQSSPKIDWVISEA 180
DB 144 YQRYESLTKNIVPFIRSSGSSRVIASGKKF:EGFQSTKLKOPRAQPGQSSPKIDWVISEA 203
QY 181 SSSNNTLDPGCTCTVFEDSELADTVANFTATVPFISIRORLND:SGVTLTDTETVYLYMD 240
DB 204 STSNNTLDPGCTCTVFEDSELADTVANFTATVPFISIRORLND:SGVTLTDTETVYLYMD 263
QY 241 CSFDTISTSTVDTKLSFPCDLTFHDEWKNYDYQSLKKYVGHGAGNPLGPTQGVYANEL 300
DB 264 CSFDTISTSTVDTKLSFPCDLTFHDEWKNYDYQSLKKYVGHGAGNPLGPTQGVYANEL 323
QY 301 IARLTHSPVHDTSSNHTLDSSPA:FPINSLTYADFSDHNGIISILFALGLYNGTKPLST 360
DB 324 IARLTHSPVHDTSSNHTLDSNPA:FPINSLTYADFSDHNGIISILFALGLYNGTKPLST 383
QY 361 TTVENITQTDGESSANTVPPFASRLYVEMMQCAEQEPVLRVLVNDRVVPPLHGCVPDALGR 420
DB 384 TTVENITQTDGESSANTVPPFASRLYVEMMQCAEQEPVLRVLVNDRVVPPLHGCVPDALGR 443
QY 421 CTGDSFVRGLSPARSGGDWAECPA 444

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Db      444 CTRDSFVXGJSFARSGGGNGECFA 467
RESULT 4
Q9HEQ0
ID      Q9HEQ0      PRELIMINARY;      PRT: 467 AA.
AC      Q9HEQ0;
DT      01-MAR-2001 (TrEMBLrel. 16, Created)
DT      01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT      01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE      Phytase
OS      Aspergillus ficuum.
OC      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC      Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX      NCBI_TaxID=5058;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Zhang J., An L., Wang Y., Yuan X.;
RJ      Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AY013315; AAG40885.1;
DR      HSSP; P34752; 1IHP.
DR      InterPro; IPR000560; HisAc_phosphatase.
DR      Pfam; PF03328; acid_phosphat_1.
DR      PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR      PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
DR      PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
SQ      SEQUENCE 467 AA; 51012 MW; 3F69A0543C0B865B CRC64;

Query Match      96.4%; Score 2249; DB 3; Length 467;
Best Local Similarity 95.3%; Pred. No. 5, 1e-164;
Matches 423; Conservative 14; Mismatches 7; Indels 0; Gaps 0;

QY      1 ASRQSSCDTVDDGYQCFSETSHLWGOYAPFFSLANESVISPEVPAGCRVTFPAQVLSRHG 60
DB      24 ASRQSSCDTVDDGYQCFSETSHLWGOYAPFFSLANESVISPEVPAGCRVTFPAQVLSRHG 63
QY      61 ARYPDSKGGKYSALIEEIQONATTEDGKYAFKTYNSLGGADLTTPGEGELVNSGKIFY 120
DB      84 ARYPDSKGGKYSALIEEIQONATTEDGKYAFKTYNSLGGADLTTPGEGELVNSGKIFY 143
QY      121 YQRYESLTRNIVPPIRSSGSSRVASGKKFIEGFQSTKLKOPRAQPGQSSPKIDVWISAE 180
DB      144 YQRYESLTRNIVPPIRSSGSSRVASGKKFIEGFQSTKLKOPRAQPGQSSPKIDVWISAE 203
QY      181 SSNNLTDPGCTVPEDSGLAOTVEANFTATVPSPICQLENLSGVTLTDTFTVYLMQMC 240
DB      204 SSNNLTDPGCTVPEDSGLAOTVEANFTATVPSPICQLENLSGVTLTDTFTVYLMQMC 263
QY      241 CSFDTISTSTVDTKLSPPFCLETHDEKWNVDYVCSLKKYVGHGAGNPLGPTQGVYANEL 300
DB      264 CSFDTISTSTVDTKLSPPFCLETHDEKWNVDYVCSLKKYVGHGAGNPLGPTQGVYANEL 323
QY      301 IARLTHSPVHDTSNHTTLOSSPATFPPLNSTLYADFSDNGITISILFALGLVNGTKPLST 360
DB      324 IARLTHSPVHDTSNHTTLOSSPATFPPLNSTLYADFSDNGITISILFALGLVNGTKPLST 383
QY      361 TTVENITQDGFSSAMTVFPASRLVEMMQCCAEQEPVRLVNDRVPLHCCPVDALGR 420
DB      384 TTVENITQDGFSSAMTVFPASRLVEMMQCCAEQEPVRLVNDRVPLHCCPVDALGR 443
QY      421 CTRDSFVRLGSLFARSGGGWAECEFA 444
DB      444 CTRDSFVRLGSLFARSGGGWAECEFA 467

RESULT 5
Q9CIT1
ID      Q9CIT1      PRELIMINARY;      PRT: 466 AA.
AC      Q9CIT1;
DT      01-JUN-2001 (TrEMBLrel. 17, Created)
DT      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE      Phytase.
OS      Aspergillus fumigatus (Sartorya fumigata).
OC      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC      Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX      NCBI_TaxID=5085;
RN      [1]
RP      SEQUENCE FROM N.A., AND SEQUENCE OF 27-37.
RC      STRAIN=ATCC 34625;
RX      MEDLINE=97288063; PubMed=9143104;

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RA Pasamontes L., Haiker M., Wyss M., Tessier M., van Loon A.P.G.M.;
 RT "Gene cloning, purification, and characterization of a heat-stable
 RT phytase from the fungus *Aspergillus fumigatus*.";
 BL Appl. Environ. Microbiol. 63:1696-1700(1997).
 CC -!- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
 CC FROM PHYTATE.
 CC -!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H₂O = D-MYO-
 CC INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 CC -!- MISCELLANEOUS: SHOWS HIGH ACTIVITY WITH 4-NITROPHENYL PHOSPHATE AT
 CC A pH RANGE OF 3 TO 5 AND WITH PHYTIC ACID AT A pH RANGE OF 2.5 TO
 CC 7.5. IT IS ABLE TO WITHSTAND TEMPERATURES UP TO 100 DEGREES
 CC CELSIUS OVER A PERIOD OF 20 MIN. WITH A LOSS OF ONLY 10% OF THE
 CC INITIAL ENZYMIC ACTIVITY.
 CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 DR EMBL: U59804; AAB96872.1; -;
 DR HSSP: P34752; 11RP.
 DR InterPro: IPR000560; HisAc_phsphtase.
 DR Pfam: PF00328; acid_phosphat_1;
 DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1;
 DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2;
 KW Hydrolase; Glycoprotein; Signal.
 FT SIGNAL 26
 FT CHAIN 27 465 3-PHYTASE A.
 FT ACT_SITE 81 81 REQUIRED FOR BINDING SUBSTRATE
 FT ACT_SITE 82 92 (BY SIMILARITY).
 FT ACT_SITE 359 359 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
 FT DISULFID 30 39 PROTON DONOR (BY SIMILARITY).
 FT DISULFID 73 412 BY SIMILARITY.
 FT DISULFID 213 463 BY SIMILARITY.
 FT DISULFID 262 280 BY SIMILARITY.
 FT DISULFID 434 442 BY SIMILARITY.
 FT CARBOHYD 104 104 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 119 119 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 205 205 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 228 228 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 337 337 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 350 350 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 374 374 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 465 AA; 50836 MW; 86FC1D9058C9B2C9 CRC64;

Query Match 68.8%; Score 1606.5; DB 3; Length 465;
 Best Local Similarity 66.4%; Pred. No. 9,4e-115;
 Matches 295; Conservative 59; Mismatches 89; Indels 1; Gaps 1;

QY 1 ASRQSCDTVDCGYQCFSETSHLWQYAFPPFSLANESVSPVAGCRVTFACVLSRHGA 60
 DB 23 SAGSKSCDTVDCGYQCFSPATSHLWQYSPFPFSLDELVSYSKLPKDCRITLVQVLSRHG 82
 QY 61 ARYPTDSKGGKYSALIEIEIQONATFDGKYPATKYNYSLGACDLTPGEQELNSGKIF 120
 DB 83 ARYPSSSKKKYKLVTAICANATDFKGPATKYNYTGLGADDLTPGEOQYNSGKIF 142
 QY 121 QRYESLTRNIVPFRSSGSRVIAAGKPFIEGFQSTKCKPRAQPGQSSPKIDVWISAS 180
 DB 143 QRYKALARSVPVPIRASSGSRVIAAGKPFIEGFQCAKADPGA-THRAAPALSVIPESE 202
 QY 181 SSNNLTDPGCTVFESSELAADVTAFTATVPSIRORLENDLSGVTLTDEVTYLMDC 240
 DB 202 EFTFNTLDHGVCCTKFEASQIGDEVAANFTALFAPO:RAFAEKHLPGVTLTDEVTYLMDC 261
 QY 241 CSFDTISTSTVDTKLSPFCDLTHDQKINVDYLSLKKYVGHGAGNPGPTCGVGVANELI 300
 DB 262 CSFETVARTSDASQSPFCQLFTHNWKKNYVLSLGGYVGHGAGNPGPTCGVGVANELI 321
 QY 301 IARLTHSPVHDTSSNHTLDSSPATFPJNSTLYADFSDHNGIISILFALGLYNGTKPLST 360
 DB 322 IARLTRSPVQDHTSTNSTLVSNPATFPJNATMYVDFSDHNSMWSIFFALGLYNGTEPLSR 382
 QY 361 TTVENITQDGFSSAWTVFFASRLYVEMMQCAQEFPLRVLVNDRVPLHGCVDALGRC 420
 DB 382 TSVESAKELDGYASVWVFFGARAYFETMCKSEKEPLVRALINDRVVPLHGCVDVKLGR 442

QY 421 CTSDSFVRGJSFARSGGWAECFA 444
 DB 442 CKLNDPVKGLSWARSGGNWGECS 465

RESULT 7
 ID Q8WZJ5 PRELIMINARY; PRI: 442 AA.
 AC Q8WZJ5;
 DT 01-VAR-2002 (TEMPREL: 20, Created;
 DT 01-VAR-2002 (TEMPREL: 20, Last sequence update;
 DT 01-VAR-2003 (TEMPREL: 23, Last annotation update;
 DE Phytase (EC 3.1.3.8) precursor (fragment).
 GN PHA3.
 OS *Aspergillus fumigatus* (Sartorya fumigatus).
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 CC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; *Aspergillus*.
 QX NCBI_TaxID=5085;
 RN [-]
 RF SEQUENCE FROM N.A.
 RC STRAIN=CCICC AF93024;
 RA Zhang G.;
 RT "Cloning of phytase gene from *Aspergillus fumigatus* and its expression
 in *Pichia pastoris*.";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ419776; CAC12529.1; -;
 DR InterPro: IPR000560; HisAc_phsphtase.
 DR Pfam: PF00328; acid_phosphat_1;
 DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1;
 DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2;
 KW Signal; Hydrolase.
 FT SIGNAL 1 1
 FT CHAIN 4 442 POTENTIAL;
 FT SIGNAL 4 442 PHYTASE.
 SQ SEQUENCE 442 AA; 48485 MW; 3FDBAC656A268514 CRC64;

Query Match 68.8%; Score 1605.5; DB 3; Length 442;
 Best Local Similarity 66.8%; Pred. No. 1e-114;
 Matches 295; Conservative 59; Mismatches 89; Indels 1; Gaps 1;

QY 2 SRQSSCOTVDCGYQCFSETSHLWQYAFPPFSLANESVSPVAGCRVTFACVLSRHGA 61
 DB 1 SAGSKSCDTVDCGYQCFSPATSHLWQYSPFPFSLDELVSYSKLPKDCRITLVQVLSRHGA 60
 QY 62 RYPTDSKGGKYSALIEIEIQONATFDGKYPATKYNYSLGACDLTPGEQELNSGKIF 121
 DB 61 RYPTSSSKKKYKLVTAICANATDFKGPATKYNYTGLGADDLTPGEOQYNSGKIF 120
 QY 122 QRYESLTRNIVPFRSSGSRVIAAGKPFIEGFQSTKCKPRAQPGQSSPKIDVWISAS 180
 DB 121 QRYKALARSVPVPIRASSGSRVIAAGKPFIEGFQCAKADPGA-THRAAPALSVIPESE 179
 QY 182 SSNNLTDPGCTVFESSELAADVTAFTATVPSIRORLENDLSGVTLTDEVTYLMDC 242
 DB 190 TENNTLDHGVCCTKFEASQIGDEVAANFTALFAPO:RAFAEKHLPGVTLTDEVTYLMDC 239
 QY 242 SFDTISTSTVDTKLSPFCDLTHDQKINVDYLSLKKYVGHGAGNPGPTCGVGVANELI 301
 DB 240 SFDTVARTSDASQSPFCQLFTHNWKKNYVLSLGGYVGHGAGNPGPTCGVGVANELI 299
 QY 302 IARLTHSPVHDTSSNHTLDSSPATFPJNSTLYADFSDHNGIISILFALGLYNGTKPLST 361
 DB 300 IARLTRSPVQDHTSTNSTLVSNPATFPJNATMYVDFSDHNSMWSIFFALGLYNGTEPLSR 359
 QY 362 TTVENITQDGFSSAWTVFFASRLYVEMMQCAQEFPLRVLVNDRVPLHGCVDALGRC 422
 DB 360 SVESAKELDGYASVWVFFGARAYFETMCKSEKEPLVRALINDRVVPLHGCVDVKLGR 419
 QY 422 TRDSFVRGJSFARSGGWAECFA 444
 DB 420 KJLNDPVKGLSWARSGGNWGECS 442

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RESULT 8
ID OC0100 PRELIMINARY; PRT: 466 AA.
AC OC0100:
DT 01-JUL-1997 (TREMUREL_04, Created)
DT 01-JUL-1997 (TREMUREL_04, Last sequence update)
DT 01-MAR-2003 (TREMUREL_23, Last annotation update)
DE 3-phosphate precursor (EC 3.1.3.8) (MYO-INOSITOL-hexakisphosphate 3-
DE phosphohydrolase) (3 phytase) (MYO-INOSITOL hexakisphosphate
DE phosphohydrolase)
OS Aspergillus terreus.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=33178;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CBS 116.46;
RA Pasamontes L., Haiker M., Henriquez Huecas M., Hug D., Mitchell D.B.,
RA Broger C., van Loon A.P.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
CC FROM PHYTATE (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H2O = D-MYO-
CC INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.
CC -2- SUBCELLULAR LOCATION: SECRETED.
CC -3- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
DR EMBL; J0412; AA058465.1;
DR HSSP; P34752; 1HP.
DR InterPro; IPR000560; HisAc phosphatase.
DR Pfam; PF00328; acid phosphatase_1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW Hydrolase; Glycoprotein; Signal.
FT SIGNAL 1 15
FT CHAIN 16 466
FT ACT_SITE 92 92
FT ACT_SITE 83 93
FT ACT_SITE 361 361
FT DISULFID 31 40
FT DISULFID 71 414
FT DISULFID 215 465
FT DISULFID 264 282
FT DISULFID 436 444
FT CARBOHYD 27 27
FT CARBOHYD 105 135
FT CARBOHYD 120 120
FT CARBOHYD 207 207
FT CARBOHYD 230 230
FT CARBOHYD 339 339
FT CARBOHYD 352 352
FT CARBOHYD 376 376
SQ SEQUENCE 466 AA; 51055 MW; F2AECBC1AF7C22C4 CRC64;

Query Match 65.1%; Score 1520; DB 3; Length 466;
Best Local Similarity 63.4%; Pred. No. 48-128;
Matches 279; Conservative 65; Mismatches 96; Indels 0; Gaps 0;

QY 4 NOSSCDTVDQGYQCFSETSHLWQYAPFFSLANESVISEVTAGCRVTFQAQVLSRHARY 63
DB 27 NNSDCTSVDRGYQCFSELSHKLWYAPFFSLANESVISEVTAGCRVTFQAQVLSRHARY 86
QY 64 PTDSKGGKYSAAIEBIQNAATFDGKYAFKTYNYSLSGADLTPFGEOELVNSGKIFQYR 123
DB 87 PTDSKTKAYAAIAAIQKNATAPGKYAFKSYNYSMSSENLPFGRLQDLQACQFYRR 146
QY 124 YSLSTENIVPFRSSGSSRVIAAGKFFEGFQSTKLKOPRACPGOSSPKIDWSEASSS 183
DB 147 YDTLRHINPFVRADSSRVHSAEKFFVEGFGNARQGGPHANPHQFSBRVDVVFEGTAY 206
QY 184 NNTLDPGTCVTFEDELACTVEANTFATFVPSIRORLENDLSGVTLTDTETVTLNDMCSF 243

207 NNTLEHSICTAFEAETVGDAAADNTFVAFAPAIKRLBADLPGVQLSAREVVNLMAXCFP 266
244 DTISTSTVDTKLSPFCDDLTTHDEWINYDLOSXKKYGGAGNPLGPTQGVGVANELLAR 303
267 ETVSJTDAAHTLSRPFCDLTAENTQYKYLSDKKYGYGGGNPLGPGVGVGNANELIAR 326
304 LTHSPVHDDTSSNHTLSSPAPFLPNSLTLYAFDSHNGHIIISLFALGLYNGTKPLSTTV 363
327 LTRSPVHDDTCVNTJDAATPFLNATLYADFSHSLVSIWALGLYNGTKP-SSQTV 386
364 ENITOTDGFSSAWTVPPASRLVENVYQCOAEPLVRLVNDRVVVELHGCPCYDALGRCTR 423
387 EDITRDGVAALKWTVPPAARALIEWQCAEAKQPLVRLVNDRVVVELHGCPCYDALGRCTR 446
424 DSFVRGCSFARSGGDWAECE 443
447 DDFVEGLSFARAGGNWAECE 466

RESULT 9
ID OC0096 PRELIMINARY; PRT: 466 AA.
AC OC0096:
DT 01-JUL-1997 (TREMUREL_04, Created)
DT 01-JUL-1997 (TREMUREL_04, Last sequence update)
DT 01-MAR-2003 (TREMUREL_23, Last annotation update)
DE Phytase (EC 3.1.3.8)
OS Talaromycetes thermophilus.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Talaromycetes.
OX NCBI_TaxID=28565;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=98007872; PubMed=9349716;
RA Pasamontes L., Haiker M., Henriquez-Huecas M., Mitchell D.B.,
RA van Loon A.P.;
RT "Cloning of the phytases from Emeticella nidulans and the thermophilic
RL fungus Talaromycetes thermophilus."
RL Biochim. Biophys. Acta 1353:217-223 (1997).
DR EMBL; U59802; AA096873.1;
DR HSSP; P34752; 1HP.
DR InterPro; IPR000560; HisAc phosphatase.
DR Pfam; PF00328; acid phosphatase_1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW Hydrolyase.
SQ SEQUENCE 466 AA; 51450 MW; FC4575B521A5C929 CRC64;

Query Match 64.1%; Score 1496.5; DB 3; Length 466;
Best Local Similarity 62.2%; Pred. No. 25e-106;
Matches 278; Conservative 58; Mismatches 106; Indels 5; Gaps 2;

QY 2 SRN----QSCOTVDQGYQCFSETSHLWQYAPFFSLANESVISEVTAGCRVTFQAQVLS 57
DB 18 SRNPHVDHSHSNTVEGGYQCFSELSHKLWYAPFFSLANESVISEVTAGCRVTFQAQVLS 77
QY 59 RHGARVFTDSKGGKYSALISLTCQNAATFDGKYAFKTYNYSLSGADLTPFGEOELVNSG 117
DB 76 RHGARVFTDSKGGKYSALISLTCQNAATFDGKYAFKTYNYSLSGADLTPFGEOELVNSG 137
QY 118 IKFYQRYESLSTENIVPFRSSGSSRVIAAGKFFEGFQSTKLKOPRACPGOSSPKIDVY 177
DB 138 IKFYQRYESLSTENIVPFRSSGSSRVIAAGKFFEGFQSTKLKOPRACPGOSSPKIDVY 197
QY 178 SEASSSNNTLDPGTCVTFEDELACTVEANTFATFVPSIRORLENDLSGVTLTDTETVTL 237
DB 198 EEGPSYNNITLDPGTCVTFEDELACTVEANTFATFVPSIRORLENDLSGVTLTDTETVTL 257
QY 238 MDKCSFDITLSTSTVDTKLSPPCDLTTHDEWINYDLOSXKKYGGAGNPLGPTQGVGVAN 297
DB 258 MDKCSFDITLSTSTVDTKLSPPCDLTTHDEWINYDLOSXKKYGGAGNPLGPTQGVGVAN 316
QY 298 NDLIARLTHSPVHDDTSSNHTLSSPAPFLNATLYADFSHSLVSIWALGLYNGTKP 357

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Db 317 RELIARMTSPVQYVTTVNTHTDSDNPATPEPLNATLYADFSNDNTMTSFAALGLYNGTAK 376
QY 358 LSTTTEVNTITODGSSAWTVPFASRLVXVMOCQAEQFLVVLVNDRVVPLHGCPVDA 417
DB 377 LSTTIKSTETGVSAAWTVFFGGRVTEMQCDSDDEPVRVLVNDRVVPLHGCEVDS 436
QY 418 LQRCRDSFVRGLSPARGSGMAECCA 444
DB 437 LGRCKRCDVRLGLSPARGSGWESCYA 463

RESULT 10
OCC0085 PRELIMINARY; PRT: 466 AA.
AC C00085;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DE 3-phytase A precursor (EC 3.1.3.8) (MYO-inositol-hexakisphosphate 3-phosphohydrolyase A) (3 phytase A) (MYO-inositol hexakisphosphate phosphohydrolyase A).
GV PHYA.
CS Aspergillus terreus.
CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
CC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
CX NCBI_TaxID=33178;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=9A1;
RX MEDLINE=97177792; PubMed=9225298;
RT Mitchell D.B., Vogel K., Weimann B.J., Pasamontes L., Leon A.P.;
RT "The phytase subfamily of histidine acid phosphatases: isolation of genes for two novel phytases from the fungi Aspergillus terreus and Myceliophthora thermophila.";
RT Microbiology 143:245-252(1997);
CC -- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE FROM PHYTATE (BY SIMILARITY);
CC -- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.
CC -- SUBCELLULAR LOCATION: SECRETED.
CC 2.5 TO 7.5, WITH MAXIMAL ACTIVITY AT PH 5.5. ALSO ACCEPT 4-NITROPHENYL PHOSPHATE AS SUBSTRATE WITH A PH OPTIMA SHIFTED TO MORE ACIDIC PH VALUES.
CC -- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
DR EMBL: U59835; AAB52507.1; -.
DR HSP: P34752; 1HP.
DR InterPro: IPR000560; HisAc_phsphtse.
DR Pfam: PF00128; acid_phosphatase.
DR PROSITE: PS00626; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW Hydrolase; Glycoprotein; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHA-N 20 466 3-PHYTASE A.
FT ACT_SITE 52 82 REQUIRED FOR BINDING SUBSTRATE (BY SIMILARITY);
FT ACT_SITE 83 83 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY);
FT ACT_SITE 361 361 PROTON DONOR (BY SIMILARITY);
FT DISULFID 31 40 BY SIMILARITY.
FT DISULFID 71 414 BY SIMILARITY.
FT DISULFID 215 465 BY SIMILARITY.
FT DISULFID 264 282 BY SIMILARITY.
FT DISULFID 436 444 BY SIMILARITY.
FT CARBOHYD 120 120 N-LINKED (GLCNAC...) (POTENTIAL);
FT CARBOHYD 207 207 N-LINKED (GLCNAC...) (POTENTIAL);
FT CARBOHYD 230 230 N-LINKED (GLCNAC...) (POTENTIAL);
FT CARBOHYD 339 339 N-LINKED (GLCNAC...) (POTENTIAL);
FT CARBOHYD 352 352 N-LINKED (GLCNAC...) (POTENTIAL);
FT CARBOHYD 376 376 N-LINKED (GLCNAC...) (POTENTIAL);
SQ SEQUENCE 466 AA; 51093 MW; 21CDB559C96AE66 CRC64;

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Query Match

54.0%; Score 1493; DB 3; Length 466;

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Best Local Similarity 62.33; Pred. No. 4,7e-106;
Matches 273; Conservative 68; X-matches 97; Indels 0; Gaps 0;
QY 6 SSCDTVDQYQCESTSH:WGOYAFPEFLANESVLSPEVPACRVTFAQVLSRHGARYPT 65
DB 29 SCNSVDHGYQCFPELSHAGLYAFYFSLQDSPPPLQVPEFEDCHITFVQVLARHARSPT 88
QY 66 DSKGKYSALIBELQCNATTFDGKYAFUKTYKYSLGADDTFFGQELVNSGIRKYQRYE 125
DB 83 HSKTRAYAAATIAAIQKSATAFPFGKYAFLOSYNYSLSBELTFEGRNQLRDLGAGFYERYN 148
QY 126 SLTRKZYPIRSSGSRVSIASKKFIEGFSQTKLXDFPACPOSSSEKIDVISEASSNNK 185
DB 149 ALTRHNPEVRATDASRVHESAEKFEVGFOTARQDHHANPHQSPFRVSVVAIPESAYNN 208
QY 186 TLDPGTCTVFEDSELACTVEANFTATFVPSIRCRLENELSGVTLTTRVTVLMEVCSPT 245
DB 209 TLEHSLCTAFESTVGGDAVANFTAVFAPAICRLAEALFGVQJSTDDVNNLMACPPET 268
QY 246 ISTTVDTKLSPFCLFTHDEMINVDYLOSJKKYVGHGAGNFGPTQGVGYANEJLARLT 305
DB 269 VSLTCDARLSPFCDLFTATEMTQNYLLSKYVGYGGNPLGPVQGVGMANELMARLT 328
QY 306 HSPVHDTSSNHTLDSSPATFFELNSTLYADFSHDNGISILFALGLYNGTKLSTTTVEN 365
DB 329 RAPVHDHTCVNNTLDASPATFFELNATLYADFSHDNLSIFWALGLYNGTAPLSQTSVS 388
QY 366 TQDGFSSAKTVPPASRLVXVMOCQAEQFLVVLVNDRVVPLHGCPVDAIGRCTROS 425
DB 389 VSGTDGYAANKVPPFAARAYVEMVQCAKEPLVRLVNDRVVPLHGCTPKLGRCKRDA 448
QY 426 FVRGLSFARGSGMAECP 443
DB 449 FVAGLSFAGAGGNWADCF 466

RESULT 11
OCC107 PRELIMINARY; PRT: 487 AA.
AC OCC107;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE 3-phytase A precursor (EC 3.1.3.8) (MYO-inositol-hexakisphosphate 3-phosphohydrolyase A) (3 phytase A) (MYO-inositol hexakisphosphate phosphohydrolyase A).
GV PHYA.
CS Thielavia heterothallica.
CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
CC Sordariales; Chaetomiaceae; Thielavia.
CX NCBI_TaxID=78579;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=97177792; PubMed=9225298;
RA Mitchell D.B., Vogel K., Weimann B.J., Pasamontes L.,
RA van Loon A.P.G.M.
RT "The phytase subfamily of histidine acid phosphatases: isolation of genes for two novel phytases from the fungi Aspergillus terreus and Myceliophthora thermophila.";
RT Microbiology 143:245-252(1997);
CC -- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE FROM PHYTATE.
CC -- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.
CC -- SUBCELLULAR LOCATION: SECRETED.
CC 3.5 TO 8.5, WITH MAXIMAL ACTIVITY WITH PHYTIC ACID AT A PH RANGE OF 3.5 TO 8.5.
CC ACCEPT 4-NITROPHENYL PHOSPHATE AS SUBSTRATE WITH A PH OPTIMA SHIFTED TO MORE ACIDIC PH VALUES.
CC -- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
DR EMBL: U59806; AAB52508.1; -.
DR HSP: P34752; 1HP.
DR InterPro: IPR000560; HisAc_phsphtse.

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DR Pfam: PF00328; acid phosphatase; 1.
DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW Hydrolase, Glycoprotein, Signal.
FT SIGNAL 1 ? POTENTIAL.
FT CHAIN 2 487 3-PHYTASE A.
FT DOMAIN 267 270 POLY-SER.
FT DOMAIN 423 433 POLY-GLY.
FT ACT_SITE 75 75 REQUIRED FOR BINDING SUBSTRATE
FT ACT_SITE 75 75 (BY SIMILARITY).
FT ACT_SITE 76 76 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
FT ACT_SITE 362 368 PROTON DONOR (BY SIMILARITY).
FT DISULFID 26 35 BY SIMILARITY.
FT DISULFID 64 421 BY SIMILARITY.
FT DISULFID 208 485 BY SIMILARITY.
FT DISULFID 260 289 BY SIMILARITY.
FT DISULFID 456 464 BY SIMILARITY.
FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 247 247 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 346 346 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 487 AA; 52537 MW; 97310EDC83D051DB CRC64;

Query Match 48.4%; Score 1129.5; DB 3; Length 487;
Best Local Similarity 45.8%; Pred. No. 3.6e-78;
Matches 217; Conservative 73; Mismatches 145; Indels 29; Gaps 4;

OY 8 CDTVDGQYQCFSETSHLMGQVAPFFSLANESVISPVPAGCRVTFACVLSRHGARYPTDS 67
DB 26 CDTPLDGFQCCGTATSHFGQVSPYSPVSE--LDASIPDDCEVTFACVLSRHGARYPTLX 83
OY 68 KKKYSAIIEICQNAITFDKYYAFKTYNYSLGADLTPFGELVNSGKIFYRYSLS 127
DB 84 RAASVYDLDRHHGAIISYGGYEFRTYDYTLGADELTRTQQQMNWSGKIFYRYREAL 143
OY 128 TRNIVPFRSSGSSRVIASGKKFIEGFQSTKLKDPRAQFGOSSPKIDVVEAGSSNNIL 187
DB 144 ARKSTPFTVATAGQDRVISAENFTQGFHSALLADRGSTVRPLFDYDMVVIPTAGANNIL 203
OY 188 DPGCTGVFDE--SELADTVEANFTATFVESIRQRIENDLSGV--TDTETVYXDMCSFD 244
DB 204 HNCLDTAFEEGYSYTGDAQDTYLSLTAGPITAPVNAKIPCAN--TDAFTVALNCLQPF 263
OY 245 TTSSTVD-----TKSPFCDFTHDEW--NYDYLSLKKYVGHGAGNPLGPTQG 293
DB 264 TVASSSSDPATADAGGNGRPLSPCFRFSSEMAAYDYLSVGKMYGYGFGNPLGPTQG 323
OY 294 VQYANELARLTHSPVHDDTSSNHTLDSPATFPLKSTLYADFSDHNGIISILPALGLYN 353
DB 324 VQVVELLARLAGVPRDGTSTNRITLDGPRFPLGRFLYADFSDHNDMNGVGLGLGAYD 383
OY 354 GTPKSTTTVENITQDGFSSAWTVPFASRLVYEMMQC-----QAEQEPFLVR 400
DB 384 GVPPDKTARROPEELGGVAASNAVPPFAARIYVKNRSGSGSGGGGGGGEQKDEMYR 443
OY 401 VLVNRRVPLHRCVVDALGRC--RDSFVRCLSPARSGCWAECPA 444
DB 444 VLVNRRVMTLKGCGADERGCMCTLERFIESWAFARGNGKWDLCFA 487

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RESULT 12

Q96VF5 ID Q96VF5 PRELIMINARY; PRT; 443 AA.

AC Q96VF5;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Phytase precursor (EC 3.1.3.26).
 GN PHYA.
 OS Trametes pubescens.
 CC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Aphyllophorales; Trametes.
 OX NCBI_TaxID=154538;

```

1.
SEQUENCE FROM N.A.
Lassen S.F., Breinholt J., Ostergaard P.R., Bruggen R., Bischoff A.,
Wys M., Fuglsang C.C.;
"Expression cloning and characterization of five novel phytases from
four basidiomycete fungi; Peniophora lycii, Agrocybe pediades, cf.
Ceriporia and Trametes pubescens."
PL Submitted (MAR-2001) to the EMBL/GenBank/CCBJ databases.
DR EMBL: AJ310700; CAC48234.1; .
DR InterPro: IPR000560; HisAc_Phsptase.
DR Pfam: PF03128; acid phosphatase; 1.
DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW Hydrolase; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 443 PHYTASE.
SQ SEQUENCE 443 AA; 47773 MW; 13D4BCE0B049D1 CRC64;

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Query Match 32.7%; Score 762.5; DB 3; Length 443;
 Best Local Similarity 39.0%; Pred. No. 4.2e-50;
 Matches 174; Conservative 70; Mismatches 167; Indels 35; Gaps 12;

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OY 3 RNOSCDTVGQYQCFSETSHLMGQVAPFFSLANESVISPVPAGCRVTFACVLSRHGAR 62
DB 28 RDTSACLDTRDQV-----QSMWSPYFPAA--TYVAP--PASCCINQVH--IQHGAR 77
OY 63 YPTDSKGGKYSALIEICQNAITFDKYYAFKTYNYSLGADLTPFGELVNSGKIFYQ 122
DB 78 FPTSGAARKRIQTAVAKLKAASNTDPLLAFTVNTYSLGQSLVELGATQSSSAGQEAFT 137
OY 123 RYBSL--TRNIVPFRSSGSSRVIASGKKFIEGFQSTKLKDPRAQFGOSSPKIDVVEAS 181
DB 136 RYSSLVADELPPVRASGSDRVVATANNWTAGF-----ALASSN--TPVLSVISEA- 189
OY 182 SSNNTLDPGTCTVFESDELADTVEANFTATFVESIRQRIENDLSGVTLTDTETVYXDMC 241
DB 190 -GNDTLDDNMCPAAGDS---DPQVQMLAQAFAPMTARLNAGAPGANLTDTDTYNLLTL 245
OY 242 SPTISTSTVOTKLSFDCFLTHDEM--N--YDY--LSLKKYVGHGAGNPLGPTQGVYANEL 300
DB 246 PFTVATE-----RRSPFCDFEELQAECAFAYKADLKPYGTYGQFGVQGVGYINEL 351
OY 301 IASLTHSPVHDDTSSNHTLDSPATFPLKSTLYADFSDHNGIISILPALGLYNKPLST 360
DB 302 IARLTACNWSCHTOTSTLDSSPETPLKRLTYADFSDHNGVAT--PSANG--FNCRAPLDP 361
OY 361 TTVEN--TQDGFSSAWTVPFASRLVYEMMQCQAEQEPFLVYVNDRVVFLHGCVPDALGP 420
DB 362 TTPD---PASTELVKKIVPFSARMVVERLDCCGAQS--VALLNDAVCPLAPCGASTSGV 416
OY 421 CTRDSFVRCLSPARSG--QWAECPA 444
DB 417 CLTDAFVESQAYARNDEGDFEKCPA 442

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RESULT 13

Q96VF5 ID Q96VF5 PRELIMINARY; PRT; 439 AA.

AC Q96VF5;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Phytase precursor (EC 3.1.3.26).
 GN PHYA.
 OS Peniophora lycii.
 CC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Aphyllophorales; Jahnnciadiaceae; Peniophora.
 OX NCBI_TaxID=154539;

1.
 SEQUENCE FROM N.A.
 Lassen S.F., Breinholt J., Ostergaard P.R., Bruggen R., Bischoff A.,
 Wys M., Fuglsang C.C.;
 "Expression cloning and characterization of five novel phytases from


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FT SIGNAL      1 19      POTENTIAL.
FT CHAIN      20 442     PHYTASE.
SQ SEQUENCE   442 AA; 47915 MW; 0464C1C691D86702 CRC64;

Query Match      31.7%; Score 139; DB 3; Length 442;
Best Local Similarity 41.0%; Pred No. 2.6e-48;
Matches 175; Conservative 64; Mismatches 154; Indels 34; Gaps 14;

Qy 25 WGVAFPFSLANESVISFEVPAGCRVTFQAQVLSRHGARYPTDSKGGKYSALIEEIQ-QN 82
Db 40 WSPYSPVFPCLAEYKA----PPAGCINQVNIQPHGARFPTSCATTIRKAGLTKLGVQN 95
Qy 53 ATTEDGYAFKTYNYSLGADDLTPGCEQLNSGKIFYORYESL-TRNIVPPIRSSGSS 141
Db 96 FT--DAKFNFIKSKYFLGNSDLVPPFGAAGSFDAGQEAFAFYKLYSKNLPPIRADGSD 153
Qy 142 RVIASGKKFIEGFOS*TKLDPRAQPGGSSPKIDVWVISEASSNNITLDPGCTCTVFESLA 201
Db 154 RVVDSATNWTAGFAS-----ASHNTVQPKNLILPQ--TGNDTIEDNMCPAAGSD-- 202
Qy 202 DTVENATATVPPIRORJENDLSGVTLTDTETVYLMCMGSDCTISTSTVDTKLSFFCDL 261
Db 203 PQVNAWLAVAP-PSITARLAAAPSVNLTDTDAENLVSLCAFLTVSKE----KKSDFTL 257
Qy 262 F--THDEWINVDYLSLKKYKYGCHGAGNPLGPTCGGVYANELLARLTHSPVHDDTSSNHTL 319
Db 258 FEGIPGSFEAPAYGGDLKDFYGTGYGELGVQGVYVNEJIALTKSAVRENTQNRIL 317
Qy 320 DSSPATPPLASTLYADFSHONGIISILFALGLYNGTKPLSTTIVENITQTDGFSSAWTP 379
Db 318 DASPVTPPLNKTFFYADFSHCNLMYAVFSANGLFQAPLS-TSVPNKFWRTSS--LYP 374
Qy 380 FASRLYVEMVCCQAEQEPVAVVJNDRVVPLHGPCVDALSGRTDSFVRGLSPARS--GG 437
Db 375 FSGRMVVERLSCFGTTK--VAVLVQDVQVPLEFCGGRNGLCTLAKEVESCTPARSDGAG 432
Qy 438 DWAECEFA 444
Db 433 DFEKCEFA 439

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Search completed: November 12, 2003, 14:32:48
Job time : 41 secs